

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 10, 2004, 11:51:21 ; Search time 5303 Seconds

(without alignments)
3210.313 Million cell updates/sec

Title: US-10-763-972-2

Perfect score: 1936

Sequence: 1 MSLILPSGRSGSRGAL.....QNKLGHPAGKRCPCGLNRS 360

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1936	100.0	1082	6	BD187416 Novel pol
2	1936	100.0	1082	6	AX458306 Sequence
3	1936	100.0	1145	9	AJ345013 Homo sapi
4	1936	100.0	1334	6	AX646427 Sequence

5	1936	100.0	1334	9	AB065670 Homo sapi
6	1936	100.0	3143	6	AX365511 Sequence
7	1936	100.0	164502	2	AC026960 Homo sapi
8	1936	100.0	167084	9	AC092999 Homo sapi
9	1936	99.3	163958	2	AC021773 Homo sapi
10	1896	97.9	1108	6	AX921825 Sequence
11	1806	93.3	1019	9	AF411108 Homo sapi
12	1798	92.9	1002	6	BD095704 Novel gua
13	1785	92.2	1020	6	BD187417 Novel pol
14	1785	92.2	1020	6	AX458308 Sequence
15	1785	92.2	1076	6	AX375230 Sequence
16	1541	79.6	850	6	AX365514 Sequence
17	1456	75.2	1140	6	AX365514 Sequence
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19	1154.5	59.6	195290	2	AC135635 Mus muscu
20	1130	58.4	250610	2	AC120742 Rattus no
21	1130	58.4	276127	2	AC116265 Rattus no
22	921	47.6	510	6	AX147768 Sequence
23	921	47.6	510	6	AX521817 Sequence
24	732	37.8	681	6	AX244718 Sequence
25	681	35.2	585	6	AX244727 Sequence
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ALIGNMENTS

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LOCUS	BD187416	Novel polypeptide.				
DEFINITION	BD187416	Novel polypeptide.				
ACCESSION	BD187416	Novel polypeptide.				
VERSION	BD187416.1	GI:32997155				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1 (bases 1 to 1082)					
AUTHORS	Fidock,M.D.					
TITLE	Novel polypeptide					
JOURNAL	Patent: JP 2003009885-A 1 14-JAN-2003;					
	Pfizer ltd (EP GB) only; Pfizer Inc (US JP EP except GB)					
COMMENT	OS homo sapiens					
	PN JP 2003009885-A/1					
	PD 14-JAN-2003					
	PF 17-DEC-2001 JP 2001382707					
	PR 18-DEC-2000 GB 0030855.1,17-JAN-2001 GB 0101222.8 PI					
	mark david fidock					
CC	CC					
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Qy	321	SerProValLeuSerPheLysGlyLysAsnArgValArgLeuGlnLysLeuArg	340
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ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1		
FEATURES	Fidock, M.D.		
source	Novel polypeptide		
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Db	61	CTCTCGAGGGAGCTCCCGGACATGGAGAGGTGGACATGAATACATCACAGGACAA	120
Qy	41	GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle	60
Db	121	GGCTCTGCGCAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC	180
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Qy	101	ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu	120
Db	301	GTGCTATTGGCCCTTCTCATATCACTACTACTAGTAGACAGGTGCCCTCTCGGGGAG	360
Qy	121	LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu	140
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LOCUS Homo sapiens P2Y2-like gene for nucleoside/nucleotide receptor.
DEFINITION
ACCESSION AJ345013
VERSION AJ345013.1 GI:34495183
KEYWORDS nucleoside/nucleotide receptor; P2Y2-like gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Bruss, M., Bonisch, H. and Kugelgen, I.
Molecular identification and functional characterization of a new G
protein-coupled nucleoside-/nucleotide receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1145)
AUTHORS Bruss, M.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Bruss M., Pharmacology and Toxicology,
University of Bonn, Reuterstrasse 2 b, D-53113, GERMANY
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VERSION			
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.			
Guanosine triphosphate-binding protein coupled receptors			
Patent: EP 1270724-A 619 02-JAN-2003;			
National Institute of Advanced Industrial Science and Technology			
(JP); Center for Advanced Science and Technology Incubation, Ltd.			
(JP)			
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LOCUS			
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Homo sapiens gene for seven transmembrane helix receptor,
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 AB065670
 VERSION
 AB065670.1 GI:21928614
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 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
 Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
 Genome-wide discovery and analysis of human seven transmembrane
 helix receptor genes
 Unpublished
 Suwa,M.
 2 (bases 1 to 1334)
 Direct Submission
 Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
 Center (CBRC), National Institute of Advanced Industrial Science
 and Technology (AIST); 2-41-6 Aomi Koto-Ku, Tokyo 135-0064, Japan
 (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
 Tel:81-3-3599-8080, Fax:81-3-3599-8081)
 This sequence is a seven transmembrane helix receptor candidate
 predicted from the whole human genome sequences using our automated
 system that contains programs of gene
 finding(GeneDecoder), sequence search, motif-domain assignment and
 transmembrane helix prediction.
 And the sequence is submitted by the collaborative project between
 [Computational Biology Research Center (CBRC), National Institute
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 QY 161 TyrArgThrArgAspHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
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 AX365511.1 GI:18873666
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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Ramakrishnan,S.
 Regulation of human p2y-like g protein-coupled receptor
 Patent: WO 0185764-A 1 15-NOV-2001;
 Bayer Aktiengesellschaft (DE)
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AC026960
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REFERENCE 1 (bases 1 to 164502)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens chromosome 3, clone RP11-170K4
Unpublished
REFERENCE 2 (bases 1 to 164502)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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Tessfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 13, 2000 this sequence version replaced gi:7328839.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu

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US-10-763-972-2 (1-360) x AC092999 (1-167084)

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DB 160981 CTCCTGGAGGAGCTCCCGGACATGGAGAGGTGGACATGATATACATACAGGAACA 161040
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Qy      321 SerProValLeuSerPheLeuGlyGlyLeuAsnArgValArgLeuLeuGlnLysLeuArg 340
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Qy      341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
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RESULT 9
LOCUS   AC021773 Homo sapiens clone RP11-12N17, WORKING DRAFT SEQUENCE, 15 unordered
DEFINITION pieces.
ACCESSION AC021773
VERSION   AC021773.6 GI:10047750
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 163958)
AUTHORS   Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE     Homo sapiens chromosome, clone RP11-12N17
JOURNAL   Unpublished
PUBLISHED 2 (bases 1 to 163958)
AUTHORS   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
           Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
           Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
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           Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
           Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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           Zimmer, A. and Zody, M.
DIRECT SUBMISSION
TITLE     Direct Submission
JOURNAL   Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Sep 10, 2000 this sequence version replaced gi:7248967.
           All repeats were identified using RepeatMasker:
           Smit, A.F.A. & Green, P. (1996-1997)
           http://ftp.genome.washington.edu/RM/RepeatMasker.html
           ----- Genome Center
           Center: Whitehead Institute/ MIT Center for Genome Research
           Center code: WIBR
           Web site: http://www-seq.wi.mit.edu
           Contact: sequence_submissions@genome.wi.mit.edu

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----- Project Information
Center project name: L3302
Center clone name: L2_N17
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152766 bases at least Q40
Consensus quality: 158075 bases at least Q30
Consensus quality: 160495 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 162558; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 7254: contig of 7254 bp in length
* 7255 7354: gap of 100 bp
* 7355 8612: contig of 1258 bp in length
* 8613 8712: gap of 100 bp
* 8713 11463: contig of 2751 bp in length
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* 11564 14507: contig of 2944 bp in length
* 14508 14607: gap of 100 bp
* 14608 22452: contig of 7845 bp in length
* 22453 35086: contig of 12534 bp in length
* 35087 35186: gap of 100 bp
* 35187 44278: contig of 9092 bp in length
* 44279 44378: gap of 100 bp
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* 76395 76494: gap of 100 bp
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* 100321 100420: gap of 100 bp
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AUTHORS			
JOURNAL			
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DEFINITION Homo sapiens GPR79 pseudogene, complete sequence.
ACCESSION AF411108
VERSION AF411108.1 GI:16566321
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1019)
AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458557
PUBMED 11574155
REFERENCE 2 (bases 1 to 1019)
AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A5, Canada
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Qy 161 TyrArgThrArgHisAlaTrrLeuGlyThrSerThrThrAlaLeuValValLeu 180
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RESULT 12
BD095704
LOCUS
DEFINITION
Novel guanosine triphosphate-bound protein-coupled receptors and
genes encoding them, and their production and use.
ACCESSION
BD095704
VERSION
BD095704.1 GI:22641292
KEYWORDS
WO 0148188-A/16.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
Matsumoto,S., Oda,T., Saito,Y., Noriyuki, Morikawa, Yoshida,K.,
Suwa,M., Sugiyama,T., Kishimoto,T., Kanzaki,K., Yasuda,S. and
Inoue,Y.
REFERENCE
Novel guanosine triphosphate-bound protein-coupled receptors and
genes encoding them, and their production and use
Patent: WO 0148188-A 16 05-JUL-2001;
HELIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO
SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU
SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO
YASUDA, YOSHIIISA INOUE
OS Homo sapiens (human)
PN WO 0148188-A/16
PD 05-JUL-2001
PF 28-DEC-2000 WO 2000JP009408
PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP OOP 101339 PI
SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI
MORIKAWA, KENJI YOSHIDA,
PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI PI
KANZAKI,
PI SHINICHIRO YASUDA, YOSHIIISA INOUE
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC
C07K16/28,
PC C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC
GOIN33/15,

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PC G01N33/50
CC Novel guanosine triphosphate-bound protein-coupled receptors
CC and genes
CC encoding them, and their production and use
FH Key Location/Qualifiers
FT source 1..1002
FT /organism='Homo sapiens (human)'
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/mol_type='genomic DNA'
/db_xref='taxon:9606'
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Best Local Similarity: 99.70% Mismatches: 1
Query Match: 92.87% Indels: 0
DB: 6 Gaps: 0
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Qy 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
Db 61 TACAAGCAAGTCTACCTCTCCCTGGCCATGATATCATCTTTATCTTAGGGCTGCCACTA 120
Qy 69 AsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
Db 121 AATGSCACTGTCTTGTGGCAGCTTCTGGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180
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Qy 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148
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Qy 149 PheLeuGlyValCysHisProLeuLeuCysSerLeuProTyrArgThrArgArgHisAlaTrp 168
Db 361 TTCCTAGTGTGTGCCACCCACTGTGTGCTGCCCTACCGGACCCGAGCATGCCCTGG 420
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SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    1 (bases 1 to 1020)
JOURNAL  Fidock, M.D.
COMMENT  Novel polypeptide
Patent: JP 2003009885-A 2 14-JAN-2003;
Pfizer Ltd (EP (GB) only), Pfizer Inc (US JP EP except GB)
OS      Homo sapiens
PN      JP 2003009885-A/2
PD      14-JAN-2003
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CC      mark david fidock
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Score:              1785.00      Matches:          337
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US-10-763-972-2 (1-360) x BD187417 (1-1020)
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Qy      121 LeuLeuCysLysLeuValHisPheLeuPheTyrlsAsnLeuTyrlsGlySerIleLeuLeu 140
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Qy      141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
Db      421 CTGACCTGCATCTCTGTGCACAGTCTCTAGGTGTGGCACCCCACTGTGTGCTGCC 480
Qy      161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
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Qy      201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrlsGlyIleValLeuThr 220
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SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    1
JOURNAL  Fidock, M.D.
FEATURES Novel polypeptide
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ORIGIN

Alignment Scores:
Pred. No.:      2,63e-152      Length:      1020
Score:          1785.00      Matches:      337
Percent Similarity: 99.12%      Conservative: 1
Best Local Similarity: 98.83%      Mismatches: 1
Query Match:      92.20%      Indels:      2
DB:              6              Gaps:      0

US-10-763-972-2 (1-360) x AX458308 (1-1020)

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Qy 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
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GenCore version 5.1.6
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Title: US-10-763-972-2

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5	420.5	21.7	984	3	US-08-513-974B-41
6	420.5	21.7	984	4	US-09-461-436B-41
7	420.5	21.7	1020	3	US-08-513-974B-370
8	420	21.7	1842	1	US-08-442-134A-1
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14	411	21.2	1571	4	US-09-016-434-1108	Sequence 1108, Ap
15	402	20.8	984	3	US-08-459-046-1	Sequence 1, Appli
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23	268	13.8	2162	3	US-09-351-198-1	Sequence 1, Appli
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27	267.5	13.8	1981	3	US-08-387-707-15	Sequence 15, Appl
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36	266.5	13.8	2453	5	PCT-US95-07180-1	Sequence 1, Appli
37	266	13.7	1020	4	US-09-170-496D-181	Sequence 181, App
38	265	13.7	1020	4	US-09-170-496D-31	Sequence 31, Appl
39	264.5	13.7	1729	4	US-09-761-962A-9	Sequence 9, Appli
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41	262.5	13.6	1334	4	US-09-761-962A-3	Sequence 3, Appli
42	262.5	13.6	1365	4	US-09-761-962A-11	Sequence 11, Appl
43	262.5	13.6	1423	4	US-09-761-962A-1	Sequence 1, Appli
44	262.5	13.6	1542	4	US-09-761-962A-4	Sequence 4, Appli
45	262.5	13.6	1610	4	US-09-761-962A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-016-434-1068
; Sequence 1068, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555

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TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1068:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1124904
US-09-016-434-1068

Alignment Scores:
Pred. No.: 1,246-37 Length: 1429
Score: 445.50 Matches: 123
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 36.18% Mismatches: 131
Query Match: 23.01% Indels: 40
DB: 4 Gaps: 9

US-10-763-972-2 (1-360) x US-09-016-434-1068 (1-1429)

QY 6 LeuPro---SerArgGlySerArgSerGlySerArgGlyAlaLeuLeuLeuGluGly 24
Db 160 CTTCCCATCTCCAGGGGGCCATGCGCAGTACAGAGTCTCCCTGTTGAGATCCCTAGGC 219
QY 25 AlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeuCysGln 44
Db 220 CTCAGC-----CCAGGCTCTGGCAGCAGTGGAGTGGAGCTGTGG 264
QY 45 PheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIlePheIleLeu 64
Db 265 TTGTATGAGGATTTCAAGTTCATCTGCTGCTGAGTATGAGTTCAGTTCCTTGTGCTG 324
QY 65 GlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSer 84
Db 325 GCCTGGGCCCTTAACGCCCAACCTATGGCTCTTCATCTCCGCCCTCCGACCTGGAT 384
QY 85 CysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---Leu 103
Db 385 GCACGGCCACCTACATGTTCCACCTGCGATGTGCACACCTTGTATGCTGTGCTGCTG 444
QY 104 ProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCys 123
Db 445 CCCACCTCATCTACTATTATGACGCCACACACCACTGGCCCTTTGGCACTGAGATCTGC 504
QY 124 LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCys 143
Db 505 AAGTTGCGCGCTTTCTTTCTATTGGAACCTCTACTGCACTGTCCTTTTCCCTCACTGC 564
QY 144 IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThr 163
Db 565 ATCAGGTGACCGCTACCTGGGATCTGCGACCTTCCGCCACTACCTGGGCCCGC 624
QY 164 ArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeuLeu 183
Db 625 CCGCTCGCGAGCGCTCTCTGCTGCGCAGTTTGGTTGGTGTGCTAGCGCGCTCGCTG 694
QY 184 ProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMet 203
Db 685 CCCAACCTGCTTTTGTACACACACACACACAGGACACCGCTCTGCTGCCATGACACC 744
QY 204 ThrSerGlnGluAsnAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGly 223
Db 745 ACTCGGCTGAAGAGTTTGACCA-CTATGTGCA-----CTTACGCTCGCGCT 791
QY 224 -----PheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGly 238
Db 792 CATGGGCTGCTCTTGGGTGCGCTCTGCTGGTCACTCTTGTGTGCTATGAGATCAATGGC 851
QY 239 GlnGluProAspGlnAlaArgGly-----GluProHisGluAsp 251
Db 852 TCGTCGCTGTATCAGGCCCTTGGCAGGCTCTGCACAGTCTGCTCTCTCGCT----- 902

```

252 ArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTrpProLeuHis 271

903 -----CCGCTCTCTCCGACCATAGCTGGTGGTCTGCTTTTGC 944

272 ProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisHisLeuLeu----- 289

945 TGTCTGCTTTCGTCCTTTCCACATCAC-----CCGACCATTTTACTACTCTGC 992

290 ---SerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMet 308

993 CAGGCTGTTGAAGCTGACTGCGGAGTACTGACATTGTCACTGGTCTATAAAGTGAC 1052

309 GluAlaSerGlyGluCysGlnLeuProGlnProSerProValLeuSerPheLysGly 328

1053 TCGGCCCTTGGCAGTGGCAGCTGCTGATCCTGCTCTACTTGTCTACTTGTCTGCTG 1112

RESULT 2

US-09-077-173D-1

; Sequence 1, Application US/09077173D

; Patent No. 6790626

; GENERAL INFORMATION:

; APPLICANT: EUROSCREEN S.A.

; APPLICANT: COMMUNI, DIDIER

; APPLICANT: PIROTON, SABINE

; APPLICANT: PARVENTIER, MARC

; APPLICANT: BOEINAENS, JEAN-MARIE

; TITLE OF INVENTION: HUMAN PYRIMIDINE RECEPTOR

; FILE REFERENCE: 9409/2112

; CURRENT APPLICATION NUMBER: US/09/077,173D

; CURRENT FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: PCT/BE96/00123

; PRIOR FILING DATE: 1996-11-21

; PRIOR APPLICATION NUMBER: EPO 95870124.5

; PRIOR FILING DATE: 1995-11-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 1

; LENGTH: 1429

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-077-173D-1

Alignment Scores:

Pred. No.: 1,246-37 Length: 1429

Score: 445.50 Matches: 123

Percent Similarity: 50.00% Conservative: 47

Best Local Similarity: 36.18% Mismatches: 131

Query Match: 23.01% Indels: 40

DB: 4 Gaps: 9

US-10-763-972-2 (1-360) x US-09-077-173D-1 (1-1429)

QY 6 LeuPro---SerArgGlySerArgSerGlySerArgGlyAlaLeuLeuLeuGluGly 24

Db 160 CTTCCCATCTCCAGGGGGCCATGCGCAGTACAGAGTCTCCCTGTTGAGATCCCTAGGC 219

QY 25 AlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeuCysGln 44

Db 220 CTCAGC-----CCAGGCTCTGGCAGCAGTGGAGTGGAGCTGTGG 264

QY 45 PheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIlePheIleLeu 64

Db 265 TTGTATGAGGATTTCAAGTTCATCTGCTGCTGAGTATGAGTTCAGTTCCTTGTGCTG 324

QY 65 GlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSer 84

Db 325 GCCTGGGCCCTTAACGCCCAACCTATGGCTCTTCATCTCCGCCCTCCGACCTGGAT 384

QY 85 CysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---Leu 103

Db 385 GCACGGCCACCTACATGTTCCACCTGCGATGTGCACACCTTGTATGCTGTGCTGCTG 444

QY 104 ProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCys 123

Db 445 CCCACCTCATCTACTATTATGACGCCACACACCACTGGCCCTTTGGCACTGAGATCTGC 504

QY 124 LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCys 143

Db 505 AAGTTGCGCGCTTTCTTTCTATTGGAACCTCTACTGCACTGTCCTTTTCCCTCACTGC 564

QY 144 IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThr 163

Db 565 ATCAGGTGACCGCTACCTGGGATCTGCGACCTTCCGCCACTACCTGGGCCCGC 624

QY 164 ArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeuLeu 183

Db 625 CCGCTCGCGAGCGCTCTCTGCTGCGCAGTTTGGTTGGTGTGCTAGCGCGCTCGCTG 694

QY 184 ProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMet 203

Db 685 CCCAACCTGCTTTTGTACACACACACACAGGACACCGCTCTGCTGCCATGACACC 744

QY 204 ThrSerGlnGluAsnAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGly 223

Db 745 ACTCGGCTGAAGAGTTTGACCA-CTATGTGCA-----CTTACGCTCGCGCT 791

QY 224 -----PheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGly 238

Db 792 CATGGGCTGCTCTTGGGTGCGCTCTGCTGGTCACTCTTGTGTGCTATGAGATCAATGGC 851

QY 239 GlnGluProAspGlnAlaArgGly-----GluProHisGluAsp 251

Db 852 TCGTCGCTGTATCAGGCCCTTGGCAGGCTCTGCACAGTCTGCTCTCTCGCT----- 902

QY 241 ProAspGlnAlaArg-----GlyGluProHisGluAspArgGlnHisSerPro 256
 Db : : : : :
 Db 917 ACTGTAAGCCAGCCTACGGAGCTCGGGCGGCT-----CCCTAGGGCCAA 964
 QY 257 SerGlnValHisProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAla 276
 Db : : : : :
 Db 965 GCGCAAGTCGCTGGCGACCATCGCGTGTCTGCTTTCGCCCTCTGCTTCCTGCC 1024
 QY 277 LeuProTyHisSerLeuLeuLeuProHisHisLeu-----SerAlaPheSer 293
 Db : : : : :
 Db 1025 ATTCCAGCTCAC-----CCGCACCTCTACTCTTCCTCCGCTCGCTGGACCT 1072
 QY 294 GlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGlu 313
 Db : : : : :
 Db 1073 CAGCTGCCACACCTCAACGCCATCAACATGGCTACAGGTTACCCGGCGCTGGCCAG 1132
 QY 314 CysGlnValLeuProGlnPro-SerProValLeuSerPheLeuGlyGlyLysAsnArgVa 333
 Db : : : : :
 Db 1133 TGCTAACAGTTG-----CCTTGACCCCGTCTCTACTTCTGCTGGCGAGGCTCGT 1186
 QY 333 lArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAla-----GlyAr 351
 Db : : : : :
 Db 1187 AGCTTTCCCGAGATGCCAAGCCA---CCCACTGGCCCGCCAGCCTGCCACCCCGGCTCG 1243
 QY 351 GlyArgCysProGlyLeuAsnArgSer 360
 Db : : : : :
 Db 1244 CCGCAGGCTG---GGCCTGGCAGATCC 1268

RESULT 4

US-09-814-915A-74
 ; Sequence 74, Application US/09814915A
 ; Patent No. 6750015
 ; GENERAL INFORMATION:
 ; APPLICANT: Horwitz, Kathryn
 ; APPLICANT: Richer, Jennifer
 ; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
 ; TITLE OF INVENTION: Thereto
 ; FILE REFERENCE: 2848-39
 ; CURRENT APPLICATION NUMBER: US/09/814,915A
 ; CURRENT FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: 60/214,870
 ; PRIOR FILING DATE: 2000-06-28
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 74
 ; LENGTH: 2025
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-814-915A-74

Alignment Scores:
 Pred. No.: 5,1e-37 Length: 2025
 Score: 442.00 Matches: 128
 Percent Similarity: 50.91% Conservative: 40
 Best Local Similarity: 38.79% Mismatches: 138
 Query Match: 22.83% Indels: 25
 DB: 4 Gaps: 10

US-10-763-972-2 (1-360) x US-09-814-915A-74 (1-2025)

QY 43 CysGlnPheSerGluLysTyLysGlnValTrpLeuSerLeuAlaTrpSerIlePhe 62
 Db : : : : :
 Db 318 TGCCGCTTCAAGGAGCTTCAAGTGTGTCTGCTGTGCTTACGCGGTGGTGC 377
 QY 63 lLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArg 82
 Db : : : : :
 Db 378 GTGCTTGGGCTGTCTGTGAACCGCGCTGTCTTCTTCTTGTGCGCGCTCAAGACC 437
 QY 83 TrpSerCysAlaThrThrTrpLeuValAsnLeuMetValAlaAspLeuLeuValLeu 102
 Db : : : : :
 Db 438 TGGATGGTCCACACATATATGTTCACTGTGCTGTGTGATGACATGATGGGCC 497
 QY 103 ---LeuProPheLeuIleThrTy-SerLeuAspArgTrpPropheGlyGluLeu 121

Db 498 TCCTTCCGCTCTGTCTATTACTACGCCCGCGGACCACTGSCCTCTAGACGGTG 557
 QY 122 LeuCysLysLeuValHisPheLeuPheTyrlleAsnLeuTyrlleGlySerIleLeuLeu 141
 Db : : : : :
 Db 558 CTCTGCAAGCTGGTGGCTTCTCTTACACCAACCTTACTGTGAGCATCTCTTCTC 617
 QY 142 ThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrl 161
 Db : : : : :
 Db 618 ACTGTGATCAGGTGACCGGTCTGGCGTCTTACACCTCTCGCTCCCTCGGCTGG 677
 QY 162 ArgThrArgArgHisAlaTrpLeuGlyThrSerThrTrpAlaLeuValLeuGln 181
 Db : : : : :
 Db 678 GCGCGCGCGCTACGCTCGCGGTGCGCGGCGGTGTGTGTGTGTGTGTGTGTGT 737
 QY 182 LeuLeuProThrLeuAlaPheSerHisThrAspTyrlleAsnGlyGlnMetIleTrpTyrl 201
 Db : : : : :
 Db 738 CAGGCCCCCGTCTTACTTTGTACACCAAGCGCGCGCGGCGGCTAACCTGCCAC 797
 QY 202 AspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTrp---GlyIleValLeuThr 220
 Db : : : : :
 Db 798 GACACTCGCACCCGAGCTCTTACGCGCTTGTGGGCTACAGCTCAGTCATGCTGGC 857
 QY 221 LeuSerGlyPheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 Db : : : : :
 Db 858 CTGCTCTTGGCGGT-GCCCTTTGGCGTATCCTTGTCTGTACGTGTCTATGGCTCGGCG 916
 QY 241 ProAspGlnAlaArg-----GlyGluProHisGluAspArgGlnHisSerPro 256
 Db : : : : :
 Db 917 ACTGTAAGCCAGCCTACGGAGCTCGGGCGGCT-----CCCTAGGGCCAA 964
 QY 257 SerGlnValHisProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAla 276
 Db : : : : :
 Db 965 GCGCAAGTCGCTGGCGACCATCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024
 QY 277 LeuProTyHisSerLeuLeuLeuProHisHisLeu-----SerAlaPheSer 293
 Db : : : : :
 Db 1025 ATTCCAGCTCAC-----CCGCACCTCTACTCTTCCTCCGCTCGCTGGACCT 1072
 QY 294 GlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGlu 313
 Db : : : : :
 Db 1073 CAGCTGCCACACCTCAACGCCATCAACATGGCTTACAGGTTACCCGGCGCTGGCCAG 1132
 QY 314 CysGlnValLeuProGlnPro-SerProValLeuSerPheLeuGlyGlyLysAsnArgVa 333
 Db : : : : :
 Db 1133 TGCTAACAGTTG-----CCTTGACCCCGTGTCTTCTTCTGCTGGCGAGGCTCGT 1186
 QY 333 lArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAla-----GlyAr 351
 Db : : : : :
 Db 1187 AGCTTTCCCGAGATGCCAAGCCA---CCCACTGGCCCGCCAGCCTGCCACCCCGGCTCG 1243
 QY 351 GlyArgCysProGlyLeuAsnArgSer 360
 Db : : : : :
 Db 1244 CCGCAGGCTG---GGCCTGGCAGATCC 1268

RESULT 5

US-08-513-974B-41
 ; Sequence 41, Application US/08513974B
 ; Patent No. 6114139
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Hosoya, Masaki
 ; APPLICANT: Fujii, Ryo
 ; APPLICANT: Ohtaki, Tetsuya
 ; APPLICANT: Fukusumi, Shoji
 ; APPLICANT: Orgi, Kazuhiro
 ; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 ; NUMBER OF SEQUENCES: 380
 ; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-41

Alignment Scores:
Pred. No.: 3,18e-35 Length: 984
Score: 420.50 Matches: 117
Percent Similarity: 45.05% Conservative: 47
Best Local Similarity: 32.14% Mismatches: 125
Query Match: 21.72% Indels: 76
DB: 3 Gaps: 9

US-10-763-972-2 (1-360) x US-08-513-974B-41 (1-984)

QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeu-----CysGln 44
|||||:|||||

Db	1	ATGGAGCAG---GACAATGGCACCACCATCCAGGCTCCAGGCTTGGCGGCCACCCACCTGGCGTC	57
QY	45	PheserGluLysTyrLysGlnValTyrLysSerLeuAlaTyrSerIleIlePheIleLeu	64
Db	58	TACCGTGAGGATTTCAAGCGACTCTCTAACCACCGGTATCTCGTGGTGGCTGGTGC	117
QY	65	GlyLeuProLeuAsnGlyThrValLeuThrPheSerTrpGlyGlnThrLysArgTrpSer	84
Db	118	GGCTGGCCACTGAACATCTGGTTCATTCGCCAGATCTCGCATCCCGCGGACCTGACC	177
QY	85	CysAlaThrThrTyrLeuValAsnMetValAlaPheLeuLeuTyrValLeu---Leu	103
Db	178	CGTTCGGCTGTGTACACCCCTGAACCTGGCATGGCGGACCTGATGATGCTGTTCATA	237
QY	104	ProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCys	123
Db	238	CCCTACTTATCTATACTACGACAGGGGACCACTGGCCCTTCGGAGACCTGGCTGC	297
QY	124	LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCys	143
Db	298	CGCTTTGTACGCTTCTCTATGCCAATCTACATGGCAGCATCTGTTCTCCTACCTGC	357
QY	144	IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---	162
Db	358	ATTAGCTTCCAGCGCTACCTGGGCATCTGCCACCCCTGGCTTCTGGCACAAGGTGGA	417
QY	163	ThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuLeu	182
Db	418	GGTCCCGCTGTGCTTGGTAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	477
QY	183	LeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAsp	202
Db	478	CTGCCACGCGAGTCTTGTGCCACAGGCATCCAGCGCAACCCGCTGTGGTGTGGTGTGG	537
QY	203	MetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSer	222
Db	538	CTGAGCCCAACCATCTCTGTCTACTCGTACCTGCCCTATGATGGCCCTCAGCGTCATC	597
QY	223	GlyPheLeu--SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProA	242
Db	598	GGCTTCTTGTGCTCCCTTCATAGCCTTACTGGCTTGTATTGTGCTG-----	641
QY	242	spGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHisProA	262
Db	642	-----CATGGCCCGCCGCTGTGTGGCCAG	666
QY	262	spHisProThr-----	265
Db	667	GATGGCCCAAGAGTCTCTGGCCCAAGAGCGGCGCAGAGCGGCTCGTATGGCTGTG	726
QY	266	-----GlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeu	284
Db	727	GTGGTGGCAGCTGTCTTTGCCATCAGCTT---CCTGCCCTTCCACATCACCAGACAGCC	783
QY	284	euProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysG	304
Db	784	TACTTGGCTGTGGCTTCCAGCGCCGCTGTCTCTTGGCCCTGTGCTGGAGACCTTCGCTGT	843
QY	304	lyLeuGlnAspMetGluAlaSerGlyGluCysGluGln-----	316
Db	844	GCCTACAAAGCAGCTCGGCCCTTCGCCAGTGTCAACAGTGTTCGTGACCCCACTTCTTTC	903
QY	317	-----LeuProGlnProSerProValLeuSerPheLysGlyGlyLysA	331
Db	904	TACTTCCACACAGAGAGTTCGGCGGC---AACCCACAGATCTCTTACAGAGCTCACAG-	961
QY	331	snArgValArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAlaGlyA	351
Db	962	-----CCAAGTGGCA	971
QY	351	rgLysArg 353	
Db	972	GAGGCAGA 979	

RESULT 6

US-09-461-436B-41
 ; Sequence 41, Application US/09461436B
 ; Patent No. 6538107
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuji Hinuma
 ; Yasuaki Ito
 ; Ryo Fujii

TITLE OF INVENTION: G Protein Coupled Receptor Protein,
 ; Production, And Use Thereof

NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ; ADDRESS: Edwards & Angell, LLP
 ; STREET: 101 Federal Street
 ; CITY: BOSTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/461,436B
 FILING DATE: 14-Dec-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513,974
 FILING DATE: 14-SEP-1995
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 APPLICATION NUMBER: 7-093989
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: 7-057186
 FILING DATE: 16-MAR-1995
 APPLICATION NUMBER: 7-007177
 FILING DATE: 20-JAN-1995
 APPLICATION NUMBER: 6-326611
 FILING DATE: 28-DEC-1994
 APPLICATION NUMBER: 6-270017
 FILING DATE: 02-NOV-1994
 APPLICATION NUMBER: 6-236357
 FILING DATE: 30-SEP-1994
 APPLICATION NUMBER: 6-236356
 FILING DATE: 30-SEP-1994
 APPLICATION NUMBER: 6-189274
 FILING DATE: 11-AUG-1994
 APPLICATION NUMBER: 6-189273
 FILING DATE: 11-AUG-1994
 APPLICATION NUMBER: 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 ; NAME: CONLIN, DAVID G.
 ; REGISTRATION NUMBER: <Unknown>
 ; REFERENCE/DOCKET NUMBER: 45753 DIV2
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-439-4444
 ; TELEFAX: 617-439-4170
 INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 984 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-461-436B-41

Alignment Scores:

Pred. No.: 3.18e-35 Length: 984
 Score: 420.50 Matches: 117

Percent Similarity: 45.05% Conservative: 47
 Best Local Similarity: 32.14% Mismatches: 125
 Query Match: 21.72% Indels: 76
 DB: 4 Gaps: 9
 US-10-763-972-2 (1-360) x US-09-461-436B-41 (1-984)
 QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeu-----CysGln 44
 Db 1 ATGGAGCAG--GACAATGGCACCATCCAGGCTCCAGGCTCCGCCCCACACCTGCCTC 57
 QY 45 PheSerGluLysTyzLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheLeu 64
 Db 58 TACCGTGAGGATTCAAGCGACTGCTGCTAACCCCGGTATCTCGTGGTGGTGGTGC 117
 QY 65 GlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSer 84
 Db 118 GGCCTGCCACTGAACATCTGCCTCATTCGCCAGATCTCGGCATCCGCCGACCCGTGACC 177
 QY 85 CysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---Leu 103
 Db 178 CGTTCGGCTGTGTACACCTGACCTGGCACTGGCGGACCTGATGATGCTGTTACTA 237
 QY 104 PropheLeuIleIleThrTyrSerLeuAspArgTrpPropheGlyGluLeuLeuCys 123
 Db 238 CCCCTACTTATCTATAACTACGCCAGAGGGGACCACTGGCCCTTCGGAGACCTGCCTGC 297
 QY 124 LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuThrCys 143
 Db 298 CGCTTTGACGCTTCTCTTATGCCAATCTACATGCGCAGCATCTCTTCTACCTGC 357
 QY 144 IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg--- 162
 Db 358 ATTAGCTCCAGCGTACTGGGCATCTGCCACCCCTGGCTCTCGCACAAGCGTGA 417
 QY 163 ThrArgArgHisAlaTrpLeuGlyThrSerThrTrpAlaLeuValValLeuGlnLeu 182
 Db 418 GGTCCCGTGTGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 477
 QY 183 LeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAsp 202
 Db 478 CTGCCACGGCAGTCTTTGCTGCCACAGGCATCCAGCGCAACCCGACCTGTGTGTACGAC 537
 QY 203 MetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSer 222
 Db 538 CTGAGCCCAACCCATCCTCTCTACTGCTACCTGCCCTATGTATGGCCCTCAGCGTATC 597
 QY 223 GlyPheLeu--SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProA 242
 Db 598 GGCCTTCTGTGCTGCCCTTCTAGCCCTTACTGCTGTGTGTGTGTGTGTGTGTGTGTGT 641
 QY 242 spGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHisProA 262
 Db 642 -----CATGGCCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
 QY 262 spHisProThr----- 265
 Db 667 GATGCCCAAGCAGGCTCTGTGCCCAAGCGCGCAGCGGCGGTCTGTATGGTGTGT 726
 QY 266 -----GlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeu 284
 Db 727 GTGGTGGCAGTGTCTTTGCCATCAGCTT---CCTGCCCTTCCACATCACCACAGACGCC 783
 QY 284 euProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysG 304
 Db 784 TACTTGGCTGTGCGCTCCACGCCCGGTGTCTTGTGCCCTGTGTGTGTGTGTGTGTGTGT 843
 QY 304 lyLeuGlnAspMetGluAlaSerGlyGluCysGluGln----- 316
 Db 844 GCCTACAAAGCAGCTCGGCCCTTCGCCAGTGTCAACAGTGTCTGTGGAGCCCTCTCTTC 903
 QY 317 -----LeuProGlnProSerProValLeuSerPheLysGlyCysAla 331
 Db 317 ----- 331

Db 904 TACTTCACACACAGAGTTCCGGCGC-AACCCACGATCTCTTACAGAGGCTCACAG- 961
Qy 331 snArgValArgLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAlaGlyA 351
Db 962 -----CCAAAGTGGA 971
Qy 351 rGlysaG 353
Db 972 GAGCAGA 979

RESULT 7
US-08-513-974B-370
Sequence 370, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513.974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 370:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1011
US-08-513-974B-370
Alignment Scores:
Pred. No.: 3,37e-35 Length: 1020
Score: 420.50 Matches: 117
Percent Similarity: 45.05% Conservative: 47
Best Local Similarity: 32.14% Mismatches: 125
Query Match: 21.72% Indels: 76
DB: 3 Gaps: 9
US-10-763-972-2 (1-360) x US-08-513-974B-370 (1-1020)
Qy 29 MetGluLysValAspMetAsnThrSerGlnGlnGlyLeu-----CysGln 44
Db 28 ATGGAGCAG--GACAATGGCACCATCCAGGCTCCAGGCTCCGCCGCCACACCTGGCTC 84
Qy 45 PheSerGluLysTyrlsGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeu 64
Db 85 TACCGTGAGGATTTCAGGACTGCTGCTAAACCCGGTATCTCGTGGTGGTGGTGC 144
Qy 65 GlyLeuProLeuAsnGlyThrValleuTrpHisSerTrpGlyGlnThrLysArgTrpser 84
Db 145 GGCTGGCCACTGACATCTGCTGCTATTGCCAGATCTCGCATCCCGCGGACCTGACC 204
Qy 85 CysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu--Leu 103
Db 205 CGTTCGGTGTACACCTGAACTGGACCTGGCAGCTGGCGGACCTGATGATGCTGTTCACTA 264
Qy 104 PropheLeuIleIleThrTyrSerLeuAspArgTrpPropheGlyGluLeuLeuCys 123
Db 265 CCCCTACTTATCTATAACTACGCAGAGGGGACCCTGGCCCTTCGAGACCTCGCTGC 324
Qy 124 LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCys 143
Db 325 CGCTTTGTACGCTTCTCTTCTATGCCAATCTACATGGCAGCATCTGTTCCTCACCTGC 384
Qy 144 IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg--- 162
Db 385 ATTAGCTTCACGCGCTACTGGGCATCTGCCACCCCTGGCTTCCTGGCACAAGCGTGA 444
Qy 163 ThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeu 182
Db 445 GGTCCGCGTGTGCTGGGTAGTGTGGAGTCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 504
Qy 183 LeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTrpAsp 202
Db 505 CTGCCACGCGCAGTCTTTGCTGCCACAGCATCCACGCCAACCCGACCTGTGTGTACGAC 564
Qy 203 MetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSer 222
Db 565 CTGAGCCCAACCATCTCTGTCTACTCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
Qy 223 GlyPheLeu--SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProA 242
Db 625 GGCTTCTTGTGCTGCTTCTATAGCCTTACTGGCTTGTATTGTGCG----- 668

242	spGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHisProA	262
669	-----CATGCCCGCGCGCTGTGCGCCAG	693
262	spHisProThr-----	265
694	GATGCCCGCAGCAGGTCTGTGGCCAGAGCGGCGCAGAGGGGCTCGTATGGCTGTG	753
266	----GlyValTrpProLeuHisProLeuPheCysAlaLeuProTrpHisSerLeuLeuL	284
754	GTGGTGGCAGCTCTCTTGCCATCAGCTT--CCTGCCTTTCACATCACCAAGACAGCC	810
284	eupProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysG	304
811	TACTTGGCTGTGCGTCCACCGCCGGTCTCTTGCCTGTGTGGAGACCTTCGGCTGT	870
304	lyLeuGlnAspMetGluAlaSerGlyGluCysGluGln-----	316
871	GCTCTACAAAGGCACCTCGGCCCTTCGCCAGTGTCAACAGTGTCTGGAGCCCATTCCTCTTC	930
317	-----LeuProGlnProSerProValLeuSerPheLysGlyGlyLysA	331
931	TACTTTCACACAAACAGAGATTCCGGCGGC-AACCCACGATCTCTTACAGAGGCTCACAG-	988
331	snArgValArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAlaGlyA	351
989	-----CCAGTGGCA	998
351	rgLysArg	353
999	GAGGCAGA	1006

RESULT 8

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US-08-442-134A-1
; Sequence 1, Application US/08442134A
; Patent No. 5596088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erd, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seitzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```


STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-513-974B-57

Alignment Scores:
Pred. No.: 2,01e-34
Score: 413.00
Percent Similarity: 48.61%
Best Local Similarity: 39.01%
Query Match: 21.33%
Indels: 22
Gaps: 8

US-10-763-972-2 (1-360) x US-08-513-974B-57 (1-984)

33 AspMetAsnThrSerGlnGlnGlnGlyLeu-----CysGlnPheSerGluLys 48
10 GACAATGGCAGGCCAGGCTCTGGGTTGCCACCCACACCTGTGTGTACCGGAGAAC 69
49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerLlePheLleLeuGlyLeuProLeu 68
70 TTCAGCAACTGCTGCTGCCACCTGTGTATTCGGGGGTGGGGGCTGGCGCTGCGCTG 129
69 AsnGlyThrValLeuTyrPheSerTyrGlnThrLysArgTyrPheSerCysAlaThrThr 88
130 AACATCTGTGTCAATACCCAGATCTGCACGTCGCCGGCGGCCCTGACCCGACGCGCTG 189
89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu--LeuProPheLeuLeu 107
190 TACACCTTAAACCTTGTCTGCTGACCTGTATATGCTCTCTCTCTCTCTCTCTCTCTCT 249
108 IleThrTyrSerLeuAspArgTyrProPheGlyGluLeuLeuCysLysLeuValHis 127
250 TACAACTATGCCCAAGGTGATCACTGGCCCTTTGGGACTTCGCTGCGGCTGGTCCGC 309
128 PheLeuPheTyrIleAsnLeuTyrGlySerLleLeuLeuLeuThrCysLysLleSerValHis 147
310 TTCCTCTTCTATGCAACCTGCAGGCGACATCTCTTCTCTACCTGCATCAGCTTCAG 369
148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgArgHis 166
370 CGCTACCTGGGCACTGCAACCCCTGGCCCTGGCACAACTGGGGGGCGCGGGCT 429
167 AlaTyrLeuGlyThrSerThrTyrTyrAlaLeuValValLeuGlnLeuLeuProThrLeu 186
430 GCCTGGCTAGTGTGTAAACGCTGTGGCTGTGGCCCTGACACCCAGTGGCTGCCACAGCC 489
187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAspMetThrSerGln 206
490 ATCTTCGCTGCCACAGGATCAGCGTAACCGCACTGTCTCTATGACTCAGCCGCT 549
207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
550 GCCCTGGCCACCCACTATATGCTTATGGCTATGCTCTCTCTCTCTCTCTCTCTCTCT 609
226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArg 246
610 CCCTTGTCTGCCCTGCTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
246 IyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrG 266
667 GATGCGCC-----CGCAGAGCTCTGCCCGAGGCGCGCTGGCAGCGCGCGCGCATG 720
266 IyValTyr-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
721 GCGC-TGGTGTGGCTGCTGCTTGGCATCAGCTT---CCTGCTTTTTCATCACCACAA 776
282 LeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
777 GACAGCTTACCTGGCAGTGGGCTCGACCGCGGGGCTCCCTGCACTGTATTGGAGGCTT 836
302 GlnCysGlyLeuGlnAspMetGluAlaSerGlyGlyCysGlnGlnLeuProGlnProSer 321
837 TGCAGCGGCTACAAAAGGACGCGCGCGCTTTGCCAGTGCACACAGCGTGTGGACCCCAT 896
322 ProValLeuSerPheLysGlyGlyLysAsnArgValArg-----LeuLeuGlnLys 338
897 CCTCTTCTAC--TTCAACCCAGAAAGTTCGCGCGGCGACCATGATGAGTCTCTCAGAAA 954
339 Leu 339
955 CTC 957

RESULT 12
US-09-461-436B-57
; Sequence 57, Application US/09461436B
; Patent No. 6538107
; GENERAL INFORMATION:

APPLICANT: Shuji Hinuma
 Yasuaki Ito
 Ryo Fujii
 TITLE OF INVENTION: G Protein Coupled Receptor Protein,
 Production, And Use Thereof
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Edwards & Angell, LLP
 STREET: 101 Federal Street
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02209
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/461,436B
 FILING DATE: 14-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/513,974
 FILING DATE: 14-SEP-1995
 APPLICATION NUMBER: PC7/JP95/01599
 FILING DATE: 10-AUG-1995
 APPLICATION NUMBER: 7-093989
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: 7-057186
 FILING DATE: 16-MAR-1995
 APPLICATION NUMBER: 7-007177
 FILING DATE: 20-JAN-1995
 APPLICATION NUMBER: 6-326611
 FILING DATE: 28-DEC-1994
 APPLICATION NUMBER: 6-270017
 FILING DATE: 02-NOV-1994
 APPLICATION NUMBER: 6-236357
 FILING DATE: 30-SEP-1994
 APPLICATION NUMBER: 6-236356
 FILING DATE: 30-SEP-1994
 APPLICATION NUMBER: 6-189274
 FILING DATE: 11-AUG-1994
 APPLICATION NUMBER: 6-189273
 FILING DATE: 11-AUG-1994
 APPLICATION NUMBER: 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: CONLIN, DAVID G.
 REGISTRATION NUMBER: <Unknown>
 REFERENCE/DOCKET NUMBER: 45753 DIV2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-439-4444
 TELEFAX: 617-439-4170
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 984 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 57:
 US-09-461-436B-57

Alignment Scores:
 Pred. No.: 2,01e-34 Length: 984
 Score: 413.00 Matches: 126
 Percent Similarity: 48.61% Conservative: 31
 Best Local Similarity: 39.01% Mismatches: 146
 Query Match: 21.33% Indels: 22
 DB: 4 Gaps: 8

US-10-763-972-2 (1-360) x US-09-461-436B-57 (1-984)

33 AspMetAsnThrSerGlnGlnGlyLeu-----CysGlnPheSerGluLys 48
 10 GACATGGCACAGCGAGCTGTGGCTTGCACCCACACCTGTGTCTACCGGAGAAC 69
 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
 70 TTCAAGCAACTGCTGCTGCCTCCACTGTATTTCGGCGGTGCTGGCGGTGCTGCGGTG 129
 69 AsnGlyThrValLeuTyrHisSerTyrGlyGlnThrLysArgTyrSerCysAlaThrThr 88
 130 AACATCTGTGTCATTACCCAGATCTGCACGCTCCCGCGGCGCTGCACCGCAGCGCGGTG 189
 89 TyrLeuValAsnLeuMetValAlaAspLeuTyrValLeu---LeuProPheLeuIle 107
 190 TACACCTAAACCTTGTCTGTGCTGACCTGTATATGCTGTCTCCTCCCTGCTCATC 249
 108 IleThrTyrSerLeuAspArgTyrProPheGlyGluLeuLeuCysLysLeuValHis 127
 250 TACAACTATGCCCAAGGTGATCCTGGCCCTTTGGCGACTTGGCTGCTGCTGCTGCTGCGC 309
 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
 310 TTCTCTTCTATGCCAACCTGCACGGCAGCATCTCTTCTCCTCAGCTGATCAGCTTCCAG 369
 148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHis 166
 370 CGCTACCTGGGCATCTGCCACCGCTGGCCCTTGGCACAACCGTGGCGGCGCGCGCT 429
 167 AlaTyrLeuGlyThrSerThrTyrAlaLeuValLeuLeuLeuLeuProThrLeu 186
 430 GCCTGGCTAGTGTGTAAACCGTGGCTGGCTGGCTGACAAACCCAGCTGCTGCCACAGCC 489
 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrAspMetThrSerGln 206
 490 ATCTTCGCTGCCACAGGCATCGATACCGCTAAGCGCATGTCTGCTATGACCTCAGCCCGCT 549
 207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuLeuLeuLeuSerGlyPheLeu--S 226
 550 GCCCTGGCCACCCACTATATGCCCTATGCCATGGCTCTCCTGCTGCTGCTGCTGCTGCTG 609
 226 exLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlnProAspGlnAlaArg 246
 610 CCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 246 IyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrG 266
 667 GATGCCCC-----GGCAGAGCCTGTGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
 266 IyValTyr-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
 721 GCCG-TGGTGGTGGCTGCTGCTGCTTGGCCATCAGCTT---CCTGCTTTTTCATCACC 776
 282 LeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
 777 GACAGCCTACCTGGCAGTGGGCTCGACCGCGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCT 836
 302 GlnCysGlyLeuGlnAspMetGluAlaSerGlyGlnCysGluGlnLeuProGlnProSer 321
 837 TGCAGCGCCCTACAAAGCAGCGCGCTTTGGCCAGTGGCCAGCGCTGCTGCTGCTGCTGCT 896
 322 ProValLeuSerPheLysGlyLysAsnArgValArg-----LeuLeuGlnLys 338
 897 CCTCTTCTAC--TTCAACCCAGAGAAGTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 954
 339 Leu 339
 955 CTC 957
 RESULT 13
 US-08-513-974B-379
 ; Sequence 379, Application US/08513974B
 ; Patent No. 6114139

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 379:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 37...1020
US-08-513-974B-379
Alignment Scores:
Pred. No.: 2,14e-34 Length: 1023
Score: 413.00 Matches: 126
Percent Similarity: 48.61% Conservative: 31
Best Local Similarity: 39.01% Mismatches: 146
Query Match: 21.33% Indels: 22
DB: 3 Gaps: 8
US-10-763-972-2 (1-360) x US-08-513-974B-379 (1-1023)
QY 33 AspMetAsnThrSerGlnGluGlnGlyLeu-----CysGlnPheSerGluLys 48
DB 46 GACAATGGCAGCCAGCGCTCTGGGTTGCCACCCACCCTGTCTTACCGGAGAAC 105
QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheLeuGlyLeuProLeu 68
DB 106 TTCAAGCAACTGCTGCTGCCACCTGTGTATCGGCGGTGCTGGCGGTGCTCCGCTG 165
QY 69 AsnGlyThrValLeuTyrPheHisTyrGlyGlnThrLysArgTyrSerCysAlaThr 88
DB 166 AACATCTGTGTATATCCAGATCTGCACGTCCCGCGGCGCCCTGACCCGACCGCGGTG 225
QY 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeu 107
DB 226 TACACCTTAAACCTTGTCTGTGCTGACCTGTATATGCTCTCTCTCTCTCTCTCTCT 285
QY 108 IleThrTyrSerLeuAspArgTyrProPheGlyGluLeuLeuCysLysLeuValHis 127
DB 286 TACAACTATGCCAAGGTGATCACTGGCCCTTTTCGCGACTTCGCGCTGCGCTCGCG 345
QY 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
DB 346 TTCTCTTTCTATGCACTTGCACGGGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 405
QY 148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHis 166
DB 406 CGCTACCTGGGCATCTGCCACCGCTGGCCCTGGCGACAAACGCTGGGGGCGCGCGCT 465
QY 167 AlaTyrLeuGlyThrSerThrTyrAlaLeuValValLeuGlnLeuLeuProThrLeu 186
DB 466 GCCTGGCTAGTGTGTGTAAACGTGTGGCTGGCGGTGACACCCAGTGTCTCTCTCTCT 525
QY 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAspMetThrSerGln 206
DB 526 ATCTTCGCTGCCACAGGCATCCAGCGTAAACCGCATGTCTGTATGACCTCAGCCGCT 585
QY 207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
DB 586 GCCCTGGCCACCCACTATATGCCCTATGCGATGGCTCTCACTGTCTCTCTCTCTCTCT 645
QY 226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArg 246
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QY 246 lyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThr 266
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QY 266 lyValTyr-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
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QY 282 LeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
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QY 302 GlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnProSer 321

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Qy 339 Leu 339
Db 991 CTC 993
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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1296659
; US-09-016-434-1108
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Query Match: 21.23% Indels: 39
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Db 346 TTCAGCAACAGCTCTGCTGCCACCTGTGTATTTCGGCGGTGGCGGTGGCTGCCGCTG 405
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Db 406 AACATCTGTGTATTACCCAGATCTGCAGCTCCGCGCGGCGCTTACCCGACGCGCGGTG 465
Qy 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu-----LeuProPheIle 107
Db 466 TACACCTTAAACCTTGTCTGTGCTGACCTGTATATGCTCTCTCCCTGCTCTCTCATC 525
Qy 108 IleThrTyrSerLeuAspArgTyrPheGlyGluLeuLeuCysLysLeuValHis 127
Db 526 TACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCTCGCGCTGTGTCGC 585
Qy 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
Db 586 TTCTCTTCTTATGCCAACCTGCAGCGCAGCATCTCTTCTTCACCTGCATCAGTTCAG 645
Qy 148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHis 166
Db 646 CGCTACCTGGGCATCTGCCACCGCTGGCCCTTGGCACAACGCTGGGGCGCGCGGCT 705
Qy 167 AlaTyrLeuGlyThrSerThrTyrAlaLeuValValLeuGlnLeuLeuProThrLeu 186
Db 706 GCCTGGCTAGTGTGTAGCGCTGTGGCTGGCTGACAAACCCAGTGCCTGCCACAGCC 765
Qy 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAspMetThrSerGln 206
Db 766 ATCTTCGCTGCCACAGGCATCCAGCTAACCGCACTGTCTGTATGACCTGCACCCGCT 825
Qy 207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuLeuLeuSerGlyPheLeu--S 226
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US-08-459-046-1
; Sequence 1, Application US/08459046
; Patent No. 6008039
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger

APPLICANT: Au-Young, Janice
 APPLICANT: Stuart, Susan G.
 TITLE OF INVENTION: A No. 6008039e1 Human Purinergic P2U Receptor
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3330 Hillview Avenue
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,046
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Luther, Barbara J.
 REGISTRATION NUMBER: 33954
 REFERENCE/DOCKET NUMBER: PF-0038 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-852-0195
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 984 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 LIBRARY: Placenta
 CLONE: 179696
 US-08-459-046-1

Alignment Scores:		
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Db	70	TTTCAGCAACTGCTCTCCACCTGTGATTCGGCGGTGCTGGCGCTGCCTCCCGCTG	129
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Db	130	AACATCTGTGTATTACCCAGATGTCACGTCCCGCGCGCCCTGACCCGACGCGCGTG	189
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Db	190	TACACCCCTAAACCTTGCTCTGCTGCCTGACCTGTATATGCTGCTCCCTGCCCTTCATC	249
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Db	250	TACAACATATGCCCAAGGTGATCACTGGCGCCCTTTGGGACTCTGCCTGCCCTGGTGGTCCG	309
Qy	128	PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis	147
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430 GCCTGGCTAGTGTGTAGCCGTGTGCTGGCGGTGACAAACCCAGTGCCTGCCACAGCC 489
187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln 206
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207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
550 GCCCTGCCACCCACTATATGCCCTATGGATGGCTCTCACTGTCATCGGCTTCCTGCTG 609
226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgG 246
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832 GCCTTTGCAGCGGCGCTACAAGGCACGGGCGGTTTGGCAGTGCACACAGCGTGTGTGAC 891
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Job time : 118 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Searched: 3611042 seqs, 2692057975 residues

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1936	100.0	1334	15	US-10-292-798-619
5	1936	100.0	3143	15	US-10-275-910-1
6	1896	97.9	1108	16	US-10-072-012-165
7	1798	92.9	1002	15	US-10-088-726-25
8	1792	92.6	1017	10	US-09-885-453-3
9	1792	92.6	1017	15	US-10-079-384-5
10	1785	92.2	1020	15	US-10-023-586B-3
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41	292	15.1	234	11	US-09-801-944B-55
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ALIGNMENTS

RESULT 1
US-10-023-586B-1
; Sequence 1, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidoock, Mark David
; TITLE OF INVENTION: No. US20030166882A1e1 Polypeptide
; FILE REFERENCE: PCT0960AGPR
; CURRENT FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-586B-1

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Pred. No.: 2,3e-211 Length: 1082
Score: 1936.00 Matches: 360
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-763-972-2 (1-360) x US-10-023-586B-1 (1-1082)

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QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
Db 421 CTGACCTGCAATCTCTGTGCACCACTTCTAGGTGTGTGCCACCATCTGTGTGGCTGCC 480
QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeu 180
Db 481 TACCGGACCGCAGGAGCATGCTGGCTGGGACACAGCACCATCTGGGCTGTGGTCTCTC 540
QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
Db 541 CAGCTGTGTGCCACACTGGGCTCTTCTCCACACGAGCTATCATCAATGCGCAGATGATCTGG 600
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
Db 601 TATGACATGACACGACAGAGAAATTTGATCGGCTTTTGGCTTACGGGCAATGTTCTGACA 660
QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
Db 661 TTGCTGGCTTTCTTTCCCTCTTGGTTCATTTTGGTGTGCTATTCTACTGATGCTCAGGAG 720
QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
Db 721 CCTGATCAGCCAGAGAGAACTCTATGAGGACAGGCAACACAGCCCGCAGGTCAT 780
QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
Db 781 CCGGACCATCTACTGTGTGTGGCTCTTCAACCTCTGTGTTTGTGGCCCTTCCATATCAC 840

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RESULT 2
US-10-763-972-1
; Sequence 1, Application US/10763972
; Publication No. US20040137500A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PCI0960B
; CURRENT APPLICATION NUMBER: US/10763,972
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-763-972-1

Alignment Scores:
Pred. No.: 2,3e-211 Length: 1082
Score: 1936.00 Matches: 360
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-763-972-2 (1-360) x US-10-763-972-1 (1-1082)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
Db 1 ATGCTGTCATTTTGGCTTCTTCCAGGGAAGCAGAAAGCGGAGCGCGTCTGGAGCTCTG 60
QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
Db 61 CTCCTGGAGGAGGAGCTCCCGGACATGAGAGAGGTGGACATGATATCATCACAGGAACAA 120
QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
Db 121 GGTCTCTGCCAGTTCTCAGAGAAGTACAAAGCAAGTCTTACCTCTCCCTGGGCTACAGTATC 180
QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTrpGlyGlnThr 80
Db 181 ATCTTTATCTAGGCTGCCACTAATGGGACATGCTCTTGTGGACATCCCTGGGCGCAACC 240
QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
Db 241 AAGCGCTGGAGCTGGCCACCATCTCTGGTGAACCTGATGTGTGGCGCCACCTGCTTTAT 300

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QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 DB 897 CCGACCATCTCTACTGTTGGTGGCTCTTACCCCTCTGTTTGTGGCTTCCATATCAC 956
 QY 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 957 TCGTCTCTTCTACTCTACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGC 1016
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 DB 1017 AGCCAGTGTGGCTTACAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCC 1076
 QY 321 SerProValLeuSerPheLeuGlyGlyLeuAsnArgValArgLeuGlnLeuValArg 340
 DB 1077 AGTCTGTACTTCTTTCAAGGGGGGCAAAATAGTCAAGCTGCTTCCAGAACTGAGG 1136
 QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
 DB 1137 CAGAACAAAGTTGGGTGAGCATCCAGCTGGGAGGAAGAGATGCCACGGTTGAACAGATCT 1196

RESULT 4

US-10-292-798-619
 ; Sequence 619, Application US/10292798
 ; Publication No. US20030235833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; PRIOR FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2070
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 619
 ; LENGTH: 1334
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: source
 ; FEATURE:
 ; LOCATION: (1)...(1334)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (201)...(715)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (834)...(1134)
 ; US-10-292-798-619

Alignment Scores:
 Pred. No.: 3,18e-211 Length: 1334
 Score: 1936.00 Matches: 360
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-763-972-2 (1-360) x US-10-292-798-619 (1-1334)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 DB 117 ATGCTGTCCATTTTGTCTTCTTCCAGGGGAAGCAGAAAGCGGAGCGCTGTGGAGCTCTG 176
 QY 21 LeuLeuGluClyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
 DB 177 CTCCTGGAGGAGCCCTCCCGGACATGGAGAGGTGGACATGAATACATCACAGGAACAA 236

QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 DB 237 GGTCTCTCCAGTTCTCAGAGAAGTACAAAGAACTACCTCTCTCTCCCTGCGCTACAGTATC 296
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTyrGlyGlnThr 80
 DB 297 AICTTTATCCCTAGGCTGCCACTAAATGGCACTGCTTTGTGGCACTCTCTGGGCGCAACC 356
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 DB 357 AAGCGCTGGAGCTGTGCCACCACTTATCTGGTGAACCTGATGGTGGCGCACTCTGCTTTAT 416
 QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspArgTrpProPheGlyCly 120
 DB 417 GTGCTATTGGCCCTTCTCTATCATCATCACCTACTACCTAGTAGACAGTGGCCCTTCGGGAG 476
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 DB 477 CTGCTCTCAAGCTGTGCTCACTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTG 536
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 DB 537 CTGACCTGCATCTCTGTGCCACAGTTCCTAGGTGTGTGCCACCACTGTGTCTGCTGCC 596
 QY 161 TyrArgThrArgHisAlaThrLeuGlyThrSerThrThrTyrAlaLeuValValLeu 180
 DB 597 TACCGACCCCGAGGATGCTGCTGGCGACACAGCACCTCTGGGCGCTGTGTGCTCTC 656
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 DB 657 CAGCTGTGCGCCACACATGCGCTTCTCCACACGAGTACATCAATGGCCAGCATCTGG 716
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 DB 717 TATGACATGACCGACCAAGAGAAATTTGATCGGCTTTTGCTTACGGCATAGTTCTGACA 776
 QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 DB 777 TTGCTGCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
 QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 DB 837 CCTGATCAAGCCAGGAGAGAACCTCATGAGACAGGCAACACAGCCCGAGCCAGTCCAT 896
 QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 DB 897 CCGGACCATCTCTACTGTTGGTGGCTCTTACCCCTCTGTTTGTGGCTTCCATATCAC 956
 QY 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 957 TCGTCTCTTCTACTCTACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGC 1016
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 DB 1017 AGCCAGTGTGGCTTACAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCC 1076
 QY 321 SerProValLeuSerPheLeuGlyGlyLeuAsnArgValArgLeuGlnLeuValArg 340
 DB 1077 AGTCTGTACTTCTTTCAAGGGGGGCAAAATAGTCAAGCTGCTTCCAGAACTGAGG 1136
 QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
 DB 1137 CAGAACAAAGTTGGGTGAGCATCCAGCTGGGAGGAAGAGATGCCACGGTTGAACAGATCT 1196

RESULT 5

US-10-275-910-1
 ; Sequence 1, Application US/10275910
 ; Publication No. US20030166142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 4974.00885
 ; CURRENT APPLICATION NUMBER: US/10/275,910


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; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/203,582
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/269,857
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (520)..(1373)
US-10-275-910-1

Alignment Scores:
Pred. No.: 12e-210 Length: 3143
Score: 1936.00 Matches: 360
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-763-972-2 (1-360) x US-10-275-910-1 (1-3143)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
DB 436 ATGCTCTCCATTTTGGTCTTCCAGGGAAGCAGAGGAGCGTCTGGAGCTCTG 495
QY 21 LeuLeuGluGlyAlaSerArgSerMetGluLysValAspMetAsnThrSerGlnGluGln 40
DB 496 CTCTCTGGAGGAGCCCTCCGGGACATGGAGAGTGGAATGATACATCAGAGNACAA 555
QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
DB 556 GGTCTCTGCCAGTTCTCAGAGAAGTACAAAGCAAGTCTACTCTCTCCCTGGCTTACAGTATC 615
QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTrpGlyGlnThr 80
DB 616 ATCTTTTATCTAGCGTGCACCTAAATGGCAGCTGTCTTGGCAGCTCTGGGGCCAAAC 675
QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
DB 676 AAGCGCTGGAGCTGTGCCACCACTATCTGTGTAACCTGATGGTGGCCGCTGCTTTAT 735
QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu 120
DB 736 GTGCTATTGCCCTTCTCATCATCACTACTACTAGTACACAGGTGGCCCTTCGGGGAG 795
QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
DB 796 CTGCTCTGCAAGCTGGTGGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCTTGCTG 855
QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
DB 856 CTGACCTGCATCTCTGTGCAACAGTCTCTAGTGTGTGCCACCACTGTGTGCTGCC 915
QY 161 TyrArgThrArgArgHisAlaTyrLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
DB 916 TACGGACCCGAGCGATGCTGTGGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 975
QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
DB 976 CAGCTGTGCCACACCTGGCTTCTCCACACGAGCTACATCAATGGCCAGATGATCTGG 1035
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
DB 1036 TATGACATGACCAAGCAAGAAATTTTGTGCGGCTTTTGTGCGGCTTGTGCGGCTTGTGCA 1095
QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
DB 1096 TTGCTGGCTTTCTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155

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RESULT 6

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US-10-072-012-165
; Sequence 165, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shamkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07

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QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
DB 1156 CTTGATCAAGCCAGGAGGAGACCTCATGAGGACAGGCAACACAGCCAGGAGTCCAT 1215
QY 261 ProAspHisProThrGlyValTyrProLeuHisProLeuPheCysAlaLeuProTyrHis 280
DB 1216 CCGGACCATCTCTACTGGTGTGGCCCTTCTACCCCTCTGTTTGTGGCCTTCCATATCAC 1275
QY 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
DB 1276 TCGCTCTCTTCTACCTACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGCG 1335
QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
DB 1336 AGCCAGTGTGGCTTACAGATATGAGGCTCTTGGTGTGTGAGCAGTGCCTTCAACCC 1395
QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
DB 1456 CAGAACCAAGTTGGGTGAGCATCCAGCTGGGAGGAAGATGCCCGAGGTTGAACAGATCT 1515

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QY 89 TyrLeuValAsnLeuMetValAlaAspLeuTyrValLeuLeuProPheLeuLeuIle 108
Db 181 TATCTGGTGAACCTGATGCTGGCCGACCTGCTTTATGCTATTCCCTTCCTCATCATC 240
QY 109 ThrTyrSerLeuAspAspArgTrpPheGlyGluLeuLeuCysIysLeuValHisPhe 128
Db 241 ACCTACTCAGTACAGAGGTGGCCCTTCGGGAGCTGCTGCAAGCTGGTGCACATTC 300
QY 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGATCTCTGTCACACAG 360
QY 149 PheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThrArgHisAlaTrp 168
Db 361 TTCCTAGGTGTGTGCCACCATGTGCTGCTGCTTACCGACCGCAGGATGCCTGG 420
QY 169 LeuGlyThrSerThrThrTrpAlaLeuValValLeuLeuLeuProThrLeuAlaPhe 188
Db 421 CTGGGACACAGCACCACCTGGGCGCTGGTGGTCTCCAGTGTGCTGCCACATGGCCCTTC 480
QY 189 SerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGlnGluAsn 208
Db 481 TCCACACGGACTACATCAATGCCAGATGATCTGGTATGACATGACCGACGCAAGAGAT 540
QY 209 PheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeuSerLeuLeu 228
Db 541 TTTGATCGGCTTTTTCCTACGGCATAGTTCTGACATGCTGGCTTTCTTTCCCTTCCT 600
QY 229 GlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgGlyGluPro 248
Db 601 GGTCAATTTTGGTGTGCTATTCATGATGTCAGAGCCTGATCAAGCCAGAGGAGAACCT 660
QY 249 HisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTrp 268
Db 661 CATGAGACAGGCAACACACCGCCAGCAGGTCCATCCGACCATCTACTGTTGTGTGG 720
QY 269 ProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisHisLeu 288
Db 721 CCTCTTCACCTCTGTTTTTGGCCCTTCATATACATCGCTCTCTTCTTACCTACCATCTG 780
QY 289 LeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMet 308
Db 781 CTCTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGCAGCCAGGTGGCCTACAAGATATG 840
QY 309 GluAlaSerGlyGluCysGlnLeuProGlnProSerProValLeuSerPheIysGly 328
Db 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCCCTCAACCCAGTCTCTGATCTTTCTTCAAGGGG 900
QY 329 GlyLysAsnArgValArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisPro 348
Db 901 GGCAAAATAGATCAGCTCTCCAGAACTGGGACAGAACAAAGTTGGTGAGCATCCA 960
QY 349 AlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
Db 961 GCTGGAGGAAGAGATGCCAGGGTTGAACAGATCT 996

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RESULT 8

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US-09-885-453-3
; Sequence 3, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCR10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1017
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA sequence
; LOCATION: (1)..(1017)
; OTHER INFORMATION: GPCR10 DNA sequence
US-09-885-453-3

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Alignment Scores:
Pred. No.: 6,55e-195 Length: 1017
Score: 1792.00 Matches: 338
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 92.56% Indels: 1
DB: 10 Gaps: 0

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US-10-763-972-2 (1-360) x US-09-885-453-3 (1-1017)

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QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgGlySerArgGlyValAlaLeu 20
Db 1 ATGTGTCATTTTGTCTTCTTCAGGGGAGCAGAGCGGAGGCCCTCGTGGAGCTCTG 60
QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
Db 61 CTCCTGGAGGAGGCTCCCGGACATGGAGAAGGTGGACATGATATACATCACAGSAA 120
QY 41 GlyLeuCysGlnPheSerGlyLysValGlnValTyrLeuSerLeuAlaTyrSerIle 60
Db 121 GGTCTCTGCCAGTCTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThr 80
Db 181 ATCTTATCTTAGGCTGCCCTAAATGGCACTGCTCTGTGGCACTCTCTGGGGCAAAACC 240
QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
Db 241 AAGCGCTGAGCTGTGCCACCATCTATCTGTGTGAACCTGTATGGTGGCGGACCTGCTTTAT 300
QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu 120
Db 301 GTGCTATTGGCTTCTCTCATCATCACCTACTACTAGATGACAGTGGCCCTTCGGGGAG 360
QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
Db 361 CTGCTCTCAAGCTGGTGCACCTCTCTGTATATCAACCTTTACGGCAGCATCTGCTGT 420
QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
Db 421 CTGACCTGCATCTCTGTGCACCATGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 480
QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
Db 481 TACCGGACCGGAGGATGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 540
QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
Db 541 CAGCTGTGTGCCACATGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 600
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
Db 601 TATGATCATGACCGACCAAGAGATTTTGTATCGCTTTTGTGTGTGTGTGTGTGTGTGTGT 660
QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
Db 661 TTGCTCTGGCTTTT-TCCCTCTCTGTCTATTGTTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
Db 720 CTGTATCAAGCCAGGAGGAGAACCTCATGAGGACAGGACAGGACAGGACAGGACAGGAC 779
QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
Db 780 CCGGACCATCTACTGTGTGTGGCTCTTACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 839

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QY 281 SerLeuLeuProHisHisLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 840 TCGCTCCCTTACCTACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTTGTATGGC 899
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluGlnLeuProGlnPro 320
 DB 900 AGCAGTGTGGCCATACAGATATGAGGCCCTCTGCTGAGTGTGAGCAGCTCCCTCAACCC 959
 QY 321 SerProValLeuSerPheLeuGlyGlyValAsnArgValArgLeuGlnLysLeu 339
 DB 960 AGTCTGTACTTCTTCAAGGGGGGCAAAATAGATCAGGCTCTCCAGAACTG 1016

RESULT 9

US-10-079-384-5
 ; Sequence 5, Application US/10079384
 ; Publication No. US20030108986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Communi, Didier
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 9409/2132
 ; CURRENT APPLICATION NUMBER: US/10/079,384
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 09/885,453
 ; PRIOR FILING DATE: 2001-06-20
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 1017
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1017)
 ; OTHER INFORMATION:
 US-10-079-384-5

Alignment Scores:
 Pred. No.: 6.55e-195 Length: 1017
 Score: 1792.00 Matches: 338
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 92.56% Indels: 1
 DB: 15 Gaps: 0

US-10-763-972-2 (1-360) x US-10-079-384-5 (1-1017)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgArgGlyAlaLeu 20
 DB 1 ATGCTGTCCATTTCCTTCTCAGGGGAAGCAGAGCGCGCTGTGGAGCTCTG 60
 QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
 DB 61 CTCTCGAGGGAGCTCCCGGACATCGAGAGGTGGACHTGATACATCACAGGACAA 120
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerIleValTyrSerIle 60
 DB 121 GGTCTCTGCCAGTCTCAGAGAAAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATC 180
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThr 80
 DB 181 ATCTTATCTAGGCTGCCACTAAATGGACATGCTTGTGGACATCTCTGGGGCCAAACC 240
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 DB 241 AAGCGTGGAGCTGTGCCACACCTATCTGCTGAACCTGATGCTGGCCGACCTCTTAT 300
 QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspAspArgTrpPheGlyGlu 120
 DB 301 GTGCTATGCGCTTCTCTCATCATCACCCTACTACTAGATGACAGGTGGCCCTTCGGGGAG 360
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 DB 361 CTGCTCTGCAAGCTGGTGCACTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTG 420

QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 DB 421 CTGACTGCATCTCTGTGCACCAAGTTCTAGGTGTGCCACCCACTGTGTTCGTGCCC 480
 QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrTrpAlaLeuValValLeu 180
 DB 481 TACCGAGCCCGCAGGCATGCTGCTGGCGCACCAACACCACTGGCCCTGTGTGCTC 540
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 DB 541 CAGCTGTGCCCCACACTGGCCCTTCCCAACAGGACTACATCATGGCCAGATGATCTGG 600
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 DB 601 TATGACATGACCCAGCAAGAGAAATTTGATCGGCTTTTGGCTACGGCATAGTTCTGACA 660
 QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGluGlu 240
 DB 661 TTGCTGGCTTTT-TCCCTCTCTGCTCATTTTGTGTGCTTATTCACGTGTCAGAG 719
 QY 241 ProAspGlnAlaAspGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 DB 720 CCTGATCAAGCCAGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGTCCAT 779
 QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 DB 780 CCGGACCATCTACTGTGTGTGGCTCTTCCACCTCTGTTTGTGGCTTCCCATATCAC 839
 QY 281 SerLeuLeuLeuProHisHisLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 840 TCGCTCTCTTACCTCACCATCTGCTTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGC 899
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluGlnLeuProGlnPro 320
 DB 900 AGCCAGTGTGGCTACAGATATGAGGCCCTCTGCTGAGTGTGAGCAGCTCCCTCAACCC 959

RESULT 10

US-10-023-586B-3
 ; Sequence 3, Application US/10023586B
 ; Publication No. US20030166882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Ltd. (EP (GB) only)
 ; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
 ; APPLICANT: Fidock, Mark David
 ; TITLE OF INVENTION: No. US20030166882A1el Polypeptide
 ; FILE REFERENCE: PCI0960AGR
 ; CURRENT APPLICATION NUMBER: US/10/023,586B
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: GB 0030855.1
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: US 60/260,563
 ; PRIOR FILING DATE: 2001-01-09
 ; PRIOR APPLICATION NUMBER: US 60/265,688
 ; PRIOR FILING DATE: 2001-02-01
 ; PRIOR APPLICATION NUMBER: GB 0101222.8
 ; PRIOR FILING DATE: 2001-01-17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 1020
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-023-586B-3

Alignment Scores:
 Pred. No.: 4.17e-194 Length: 1020
 Score: 1785.00 Matches: 337
 Percent Similarity: 99.12% Conservative: 1

Best Local Similarity: 98.83%		Matches: 1	
Query Match: 92.20%		Indels: 2	
DB: 15		Gaps: 0	
US-10-763-972-2 (1-360) x US-10-023-586B-3 (1-1020)			
Qy	1	MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu	20
Db	1	ATGCTGTCCATTTTGTCTTCCTCCAGGGAAGCAGAGCGGAGCGTCTGGAGCTCTG	60
Qy	21	LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln	40
Db	61	CTCCTGGAGGAGCCTCCCGGACATGGAGAGGTGGACATGAATACATCAGAGAACAA	120
Qy	41	GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle	60
Db	121	GGTCTCTGCCAGTTCACAGAGTACACAGCAAGTCTACTCTCCCTGGCCCTACAGTATC	180
Qy	61	IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTrpGlyGlnThr	80
Db	181	ATCTTTTATCTAGGCTGCGCACCACTAATGGCACTGTCTTGTGGCACTCTCGGGCCAAACC	240
Qy	81	LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuTyr	100
Db	241	AAGCGCTGAGCTGTGCCACCACTATCTGGTGAACCTGATGTGGCCGACCTGCTTTAT	300
Qy	101	ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu	120
Db	301	GTGCTATTGGCTTCCTCATCATCACTACTAGATGACAGGTGGCCCTTCGGGAG	360
Qy	121	LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu	140
Db	361	CTGCTCTGCAAGCTGTGGCACTTCCTGTTCTATATCAACCTTTACGGCAGCATCTGCTG	420
Qy	141	LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro	160
Db	421	CTGACCTGTGATCTCTGTGCCACCACTTCTAGGTGTGGCACCACTGTGTCTGGTGGCC	480
Qy	161	TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuLeu	180
Db	481	TACCGGACCCGAGGAGCATGCTGGCTGGGACACAGCACCACTGGGCCCTGGTGTCTCT	540
Qy	181	GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp	200
Db	541	CAGCTGTGCCCACTCTGGCTTCTCCACACGGACTTACATCAATGGCCAGATGATCTGG	600
Qy	201	TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr	220
Db	601	TATGACATGACCAAGCAAGAGATTTTGATCGGCTTTTGGCTTACGGCATAGTCTTGACA	660
Qy	221	LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG	240
Db	661	TTGTCTGGCTTCTTCTCCCTCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTTCAGG	720
Qy	240	IuProAspGlnAlaArgGlyClnuProHisGluAspArgGlnHisSerProSerGlnValH	260
Db	721	AGCCTGATCAAGCCAGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGTCC	780
Qy	260	IsProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrH	280
Db	781	ATCCGACCATCTACTGTGTGGGCTCTTCAACCCTCTGTTTGTGGCCCTTCCATATC	840
Qy	280	IsSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG	300
Db	841	ACTCGCTCTTCTACCTCACCATCTGCTTCTTGCTTTCTCAGGACTGCCAGCTCTTGATG	900
Qy	300	IySerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnP	320
Db	901	GCACCCAGTGTGGCCTACAAGATATGAGGACCTCTGGTGTGAGTGTGAGCAGCTGCCCTCAAC	960
Qy	320	roSerProValLeuSerPheIyGlyGlyLysAsnArgValArgLeuLeuGlnLysLeu	339
Db	961	CCAGTCTGTGATTTCTTTCAAGGGGGGCAAAATAGATGAGCTCTCTCCAGAACTG	1019

RESULT 11			
US-10-763-972-3			
; Sequence 3, Application US/10763972			
; Publication No. US20040137500A1			
; GENERAL INFORMATION:			
; APPLICANT: PFIZER INC.			
; APPLICANT: Fadock, Mark David			
; TITLE OF INVENTION: Novel Polypeptide			
; FILE REFERENCE: PC10960B			
; CURRENT APPLICATION NUMBER: US/10/763,972			
; CURRENT FILING DATE: 2004-01-23			
; PRIOR APPLICATION NUMBER: GB 0030855.1			
; PRIOR FILING DATE: 2000-12-18			
; PRIOR APPLICATION NUMBER: US 60/260,563			
; PRIOR FILING DATE: 2001-01-09			
; PRIOR APPLICATION NUMBER: US 60/265,688			
; PRIOR FILING DATE: 2001-02-01			
; PRIOR APPLICATION NUMBER: GB 0101222.8			
; PRIOR FILING DATE: 2001-01-17			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 3			
; LENGTH: 1020			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-763-972-3			
Alignment Scores:		Length: 1020	
Pred. No.:		Matches: 337	
Score:		Conservative: 1	
Percent Similarity:		Mismatches: 1	
Best Local Similarity:		Indels: 2	
Query Match:		Gaps: 0	
DB:		17	
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Qy	1	MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu	20
Db	1	ATGCTGTCCATTTTGTCTTCCTCCAGGGAAGCAGAGCGGAGCGTCTGGAGCTCTG	60
Qy	21	LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln	40
Db	61	CTCCTGGAGGAGCCTCCCGGACATGGAGAGGTGGACATGAATACATCAGAGAACAA	120
Qy	41	GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle	60
Db	121	GGTCTCTGCCAGTTCACAGAGTACACAGCAAGTCTACTCTCCCTGGCCCTACAGTATC	180
Qy	61	IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTrpGlyGlnThr	80
Db	181	ATCTTTTATCTAGGCTGCGCACCACTAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACCC	240
Qy	81	LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuTyr	100
Db	241	AAGCGCTGAGCTGTGCCACCACTATCTGGTGAACCTGATGGTGGCCGACCTGCTTTAT	300
Qy	101	ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu	120
Db	301	GTGCTATTGGCTTCCTCATCATCACTACTAGATGACAGGTGGCCCTTCGGGAG	360
Qy	121	LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu	140
Db	361	CTGCTCTGCAAGCTGTGGCACTTCCTGTTCTATATCAACCTTTACGGCAGCATCTGCTG	420
Qy	141	LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro	160
Db	421	CTGACCTGTGATCTCTGTGCCACCACTTCTAGGTGTGGCACCACTGTGTCTGGTGGCC	480
Qy	161	TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuLeu	180
Db	481	TACCGGACCCGAGGAGCATGCTGGCTGGGACACAGCACCACTGGGCCCTGGTGTCTCT	540
Qy	181	GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp	200
Db	541	CAGCTGTGCCCACTCTGGCTTCTCCACACGGACTTACATCAATGGCCAGATGATCTGG	600
Qy	201	TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr	220
Db	601	TATGACATGACCAAGCAAGAGATTTTGATCGGCTTTTGGCTTACGGCATAGTCTTGACA	660
Qy	221	LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG	240
Db	661	TTGTCTGGCTTCTTCTCCCTCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTTCAGG	720
Qy	240	IuProAspGlnAlaArgGlyClnuProHisGluAspArgGlnHisSerProSerGlnValH	260
Db	721	AGCCTGATCAAGCCAGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGTCC	780
Qy	260	IsProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrH	280
Db	781	ATCCGACCATCTACTGTGTGGGCTCTTCAACCCTCTGTTTGTGGCCCTTCCATATC	840
Qy	280	IsSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG	300
Db	841	ACTCGCTCTTCTACCTCACCATCTGCTTCTTGCTTTCTCAGGACTGCCAGCTCTTGATG	900
Qy	300	IySerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnP	320
Db	901	GCACCCAGTGTGGCCTACAAGATATGAGGACCTCTGGTGTGAGTGTGAGCAGCTGCCCTCAAC	960
Qy	320	roSerProValLeuSerPheIyGlyGlyLysAsnArgValArgLeuLeuGlnLysLeu	339
Db	961	CCAGTCTGTGATTTCTTTCAAGGGGGGCAAAATAGATGAGCTCTCTCCAGAACTG	1019

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QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyr 200
DB 541 CAGCTGCTGCCACACACTGGCTTCTCCACACGAGTACATCATGGCCAGATGATCTGG 600
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
DB 601 TATGACATGACACAGCCAGAGAAATTTGATCGGCTTTTGGCTACGGCAGTAGTTCTGACA 660
QY 221 LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG 240
DB 661 TTGCTGGCTTCTTCCCTCTTGGTCAATTTGGTGCTATTACCTGATGGTCAGG 720
QY 240 LuProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValH 260
DB 721 AGCCTGATCAAGCCAGAGGAGACCTCATGAGGACAGCAACACAGCCGAGCCAGGTCC 780
QY 260 isProAspHisProThrGlyValTyrProLeuHisProLeuPheCysAlaLeuProTyrH 280
DB 781 ATCCGGACCATCCCTACTGCTGTGGCTCTTACCTCTGTTTGGCTTCTCCATATC 840
QY 280 isSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG 300
DB 841 ACTCGCTCCTTCTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATG 900
QY 300 lySerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnP 320
DB 901 GCACCCAGTGTGGCTTCAAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCCCTCAAC 960
QY 320 roSerProValLeuSerPheLysGlyGlyLysAsnArgValArgLeuGlnLysLeu 339
DB 961 CCAGTCTGTAATTCTTTCAGGGGGGCAAAATAGAGTACAGCTCCTCCAGAACTG 1019

RESULT 12
US-10-333-946-20
; Sequence 20, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAI, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RANKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Navinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1076

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CB1
US-10-333-946-20

Alignment Scores:
Pred. No.: 4,53e-194 Length: 1076
Score: 1785.00 Matches: 337
Percent Similarity: 99.12% Conservatives: 1
Best Local Similarity: 99.83% Mismatches: 1
Query Match: 92.20% Indels: 2
DB: 16 Gaps: 0

US-10-763-972-2 (1-360) x US-10-333-946-20 (1-1076)

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QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgArgGlyAlaLeu 20
DB 57 ATGCTGTCCATTTTCTCTTCCAGGGAAGCAGAGCGGAGCCGTCGTGGAGCTCTG 116
QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGlnGln 40
DB 117 CTCCTGGAGGGAGGCTCCCGGGACATGGAGAAGGTGGACATGAATACATCACAGGAACA 176
QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
DB 177 GGTCTCTGCCAGTTCTCAGAGAAGTACAAAGCAAGTCTACCTCTCCCTGGCCCTCAGTATC 236
QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTyrGlyGlnThr 80
DB 237 ATCTTTATCTTAGGGCTGCCATAATGGCACTGTCTTGTGGCACTCTCTGGGGCAAAACC 296
QY 81 LysArgTyrSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
DB 297 AAGCGCTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGTGGCGCCAGCTGCTTTAT 356
QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspArgTyrProPheGlyGlu 120
DB 357 GTGCTATTGGCCCTTCTCTCATCATCCTACTCATCTAGATGACAGTGGCCCTTCGGGAG 416
QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
DB 417 CTGCTCTCAAGCTGGTGCACTTCTCTGTCTATATCAACCTTTTACGGCAGCATCTGCTG 476
QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
DB 477 CTGACCTGCATCTCTGTGCACCACTTCTAGGTGTGGCACCACCTGTGTGCTGCTGCC 536
QY 161 TyrArgThrArgArgHisAlaTyrLeuGlyThrSerThrThrTyrAlaLeuValValLeu 180
DB 537 TACCGGACCCGAGGATGCTGCTGGCCACAGCACCCTGGGCCCTGGTGGTCTC 596
QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyr 200
DB 597 CAGCTGTGCCACACATGGCCCTTCTCCACACGAGCTACATCATATGGCCAGATGATCGG 656
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
DB 657 TATGACATGACACAGCCAGAGAAATTTGATCGGCTTTTGGCTTACGGCATAGTTCTGACA 716
QY 221 LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG 240
DB 717 TTGCTGGCTTCTTCTCCCTCTCTTGGTCAATTTGGTGCTATTACCTGATGGTCTCAGG 776
QY 240 LuProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValH 260
DB 777 AGCCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGCAACACAGCCGAGCCAGGTCC 836
QY 260 isProAspHisProThrGlyValTyrProLeuHisProLeuPheCysAlaLeuProTyrH 280
DB 837 ATCCGGACCATCTCTACTGCTGTGGCTCTTCCACCTCTGTTTGTGGCTTCTCCATATC 896

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QY 280 isSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG 300
 Db 897 ACTCGCTCTTCTACCTACCATCTGCTTTCTGCTTTCTCAGACTGCCAGCTCTGATG 956
 QY 300 lSerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGlnGlnLeuProGlnP 320
 Db 957 GCACCCAGTGTGGCTTACAGATATGAGGCTCTGGTGGTGTGAGCAGCTGCCCTCAAC 1016
 QY 320 roSerProValLeuSerPheLysGlyGlyAsnArgValArgLeuLeuGlnLysLeu 339
 Db 1017 CCAGTCTCTACTTCTTTCAAGGGGGCAAAATAGATCAGGCTCTCCACAGAACTG 1075
 RESULT 13
 US-10-275-910-4
 ; Sequence 4, Application US/10275910
 ; Publication No. US20030166142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 4974.00885
 ; CURRENT APPLICATION NUMBER: US 10/275,910
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: US 60/203,582
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: US 60/269,857
 ; PRIOR FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 850
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-275-910-4
 Alignment Scores:
 Pred. No.: 2,81e-166 Length: 850
 Score: 1541.00 Matches: 283
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 79.60% Indels: 0
 DB: 15 Gaps: 0
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 QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
 Db 61 TACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
 QY 69 AsnGlyThrValLeuThrHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
 Db 121 AATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACAGCGCTGGAGCTGTGCCACACC 180
 QY 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeuLeuProPheLeuIleIle 108
 Db 181 TAUCGTGTACACCTAGTGGTGGCGGACCTGTTATGTGCTATTGCCCTTCCTCATCATC 240
 QY 109 ThrTyrSerLeuAspAspA-gfTrpProPheGlyGluLeuLeuCysLysLeuValHisPhe 128
 Db 241 ACCTACTCACTAGATGACAGTGGCCCTCTGGGGAGCTGTCTGCAAGCTGGTGCACTTC 300
 QY 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148
 Db 301 CTGTTCATATCAACCTTTACGGCAGCATCTCTGCTGACCTGATCTCTGTGGCACCAG 360
 QY 149 PheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThrArgA-gHisAlaTrp 168
 Db 361 TTCCTAGTGTGGCCACCACTGTTGCTGGCTGCCCTACCGACCCGAGCATGCCCTGG 420
 QY 169 LeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeuLeuProThrLeuAlaPhe 188

Db 421 CTGGGCACACAGACACCTGGGCCCTGGTGGTCTCTCCAGCTGTGCCACACTGGGCTTC 480
 QY 189 SerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGlnGluAsn 208
 Db 481 TCCACACAGGACTACATCAATGGCCAGATGATCTGGTATCAGCATGACGCCAAGAGAT 540
 QY 209 PheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeuSerLeuLeu 228
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 QY 249 HisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTrp 268
 Db 661 CATGAGACAGGCAACACAGCCGAGCAGTCCATCCGACCATCTACTGTGTGTGG 720
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 QY 309 GluAlaSer 311
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 ; Sequence 6, Application US/10275910
 ; Publication No. US20030166142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 4974.00885
 ; CURRENT APPLICATION NUMBER: US 10/275,910
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: US 60/203,582
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: US 60/269,857
 ; PRIOR FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 851
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
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 Score: 1541.00 Matches: 283
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 79.60% Indels: 0
 DB: 15 Gaps: 0
 US-10-763-972-2 (1-360) x US-10-275-910-6 (1-851)
 QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeuCysGlnPheSerGluLys 48
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 QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
 Db 61 TACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
 QY 69 AsnGlyThrValLeuThrHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88

Db 121 AATGCACTGCTTTGTGGCACTCTCTGGGCGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180
Qy 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeuLeuProPheLeuLeuIle 108
Db 181 TATCTGGTGAACCTGATGGTGGCGACTGCTTTATGTGCTATTGGCCCTTCCTCATCATC 240
Qy 109 ThrTyrSerLeuAspArgTyrProPheGlyLeuLeuLeuCysLysLeuValHisPhe 128
Db 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCACCTC 300
Qy 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148
Db 301 CTGTTCATATCAACCTTTACGGCAGATCTCTGCTGACCTGCTGCTGCTGCTGCTGCTG 360
Qy 149 PheLeuGlyValCysHisProLeuLeuCysSerLeuProTyrArgThrArgHisAlaTyr 168
Db 361 TTCCTAGTGTGGCCACCCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 169 LeuGlyThrSerThrThrTyrAlaLeuValValLeuGlnLeuLeuProThrLeuAlaPhe 188
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Qy 189 SerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAspMetThrSerGlnGluAsn 208
Db 481 TCCACACGGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACCGCCAGAGAA 540
Qy 209 PheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeuSerLeuLeu 228
Db 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGCATTTGTGCTGCTGCTGCTGCTGCT 600
Qy 229 GlyHisPheGlyValLeuPheThrAspGlyGlnLeuProAspGlnAlaArgGlyGluPro 248
Db 601 GGTCACTTTGGTGGCTATTCATGATGTCAGAGGCTGATCAAGCCAGAGAGAACCT 660
Qy 249 HisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTyr 268
Db 661 CATGAGGACAGGCAACACAGCCGAGCCAGGTCCATCCGACCATCTACTGTGTGTGG 720
Qy 269 ProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisHisLeu 288
Db 721 CCTCTTCACCTCTGTTTGGCGCTTCCATATCATCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 289 LeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMet 308
Db 781 CTCTCTCTTTCAGGACTGCCAGCTCTTGAATGGCAGCCAGTGTGGCCTACAGATATG 840
Qy 309 GluAlaSer 311
Db 841 GAGGCTCTCT 849

RESULT 15

US-09-782-974C-13
; Sequence 13, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19

; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-13
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Score: 921.00 Matches: 170
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.57% Indels: 0
DB: 10 Gaps: 0
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Qy 103 LeuProPheLeuIleIleThrTyrSerLeuAspArgThrProPheGlyGluLeuLeu 122
Db 61 TTGCCCTCTCTCATCATCACCTACTACTAGTACAGGTGGCCCTTCGGGGAGCTGCTC 120
Qy 123 CysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThr 142
Db 121 TGCAGCTGTGGCCAGCTTCTCTTCTATATCAACCTTTACGCGACGATCTCTGCTGCTC 180
Qy 143 CysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg 162
Db 181 TGCATCTCTGTGGCCAGCTTCTTAGGTGTGGCCACCCACTGTGTGCTGCTGCTACCGG 240
Qy 163 ThrArgArgHisAlaTyrLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeu 182
Db 241 ACCGCGAGGCAATGCTGCTGGCCAGCCAGCCACCTGGGCGCTGTGTGCTCTCCAGCTG 300
Qy 183 LeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAsp 202
Db 301 CTGCCACACCTGGCGCTTCTCCACACCGGACTACATCAATGGCCAGATGATCTGGTATGAC 360
Qy 203 MetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSer 222
Db 361 ATGACACGCCAAGAGAATTTGATCGGCTTTTGGCTTACGCGATAGTCTTGACATTTGCT 420
Qy 223 GlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAsp 242
Db 421 GGCCTTCTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 243 GlnAlaArgGlyGluProHisGluAspArg 252
Db 481 CAAGCCAGGAGAGAACCTCATGAGGACAGG 510

Search completed: November 10, 2004, 14:57:07
Job time : 632 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 10, 2004, 10:44:11 ; Search time 3860 Seconds

(without alignments)
3398.524 Million cell updates/sec

Title: US-10-763-972-2

Perfect score: 1936

Sequence: 1 MSLILPSRSGSRGAL.....QNKLGHPAGKRCPCPLNRS 360

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cg2_1/USPFO.spool/US10763972/runat_04112004_093314_8797/app.query.fasta_1.519
-DB=EST -QMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOPCU=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USPR=US10763972 @CGN 1 1 3437 @runat_04112004_093314_8797 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	460.5	23.8	4439	3 AK076364	AK076364 Mus muscu
2	455	23.5	693	6 CD217676	CD217676 pgrin.pk0
3	420.5	21.7	987	9 AY400799	AY400799 Mus muscu
4	416	21.5	987	9 AY400798	AY400798 Pan trogl
5	414.5	21.4	1425	3 CR624871	CR624871 full-leng
6	414.5	21.4	2542	3 AK017378	AK017378 Mus muscu
7	414.5	21.4	3001	3 AK005013	AK005013 Mus muscu
8	411	21.2	987	9 AY400797	AY400797 Homo sapi
9	411	21.2	1515	3 CR612681	CR612681 full-leng

10	411	21.2	1532	3	CR618945	full-leng
11	411	21.2	1564	3	CR626266	full-leng
12	411	21.2	1589	3	CR626754	full-leng
13	411	21.2	1592	3	CR605588	full-leng
14	411	21.2	1594	3	CR606834	full-leng
15	411	21.2	1638	3	CR617080	full-leng
16	411	21.2	1651	3	CR597500	full-leng
17	411	21.2	1686	3	CR626706	full-leng
18	411	21.2	1690	3	CR598765	full-leng
19	398	20.6	845	5	EX740173	EX740173
20	397.5	20.5	1035	5	EX739990	EX379990
21	396.5	20.5	1042	5	EX397649	EX397649
22	387	20.0	639	6	CA352828	624212 NC
23	386	19.9	925	5	EX704227	EX704227
24	380	19.6	828	6	CD110272	AGENCOURT
25	380	19.6	970	5	EX385626	EX385626
26	380	19.6	993	5	EX394202	EX394202
27	380	19.6	1013	3	CR614658	full-leng
28	380	19.6	1065	5	EX337204	EX337204
29	380	19.6	1090	3	CR598708	full-leng
30	378	19.5	851	4	BI833118	603090834
31	370	19.1	955	5	EX354044	EX354044
32	361.5	18.7	972	5	EX337012	EX337012
33	360.5	18.6	641	5	EQ396255	EQ396255 NISC ng19
34	359.5	18.6	627	1	AL675845	AL675845
35	357	18.4	606	8	AZ953874	2M0219117
36	355.5	18.4	730	7	CK359970	AGENCOURT
37	355.5	18.4	1063	4	BM918491	BM918491 AGENCOURT
38	354	18.3	804	7	BP688283	BP688283
39	353.5	18.3	1054	5	EX364429	EX364429
40	351.5	18.2	1815	5	EX210812	EX210812 RJA041C08
41	350	18.1	916	5	EX396836	EX396836
42	348.5	18.0	1014	5	EX381745	EX381745
43	345.5	17.8	862	7	CN839909	CN839909 AGENCOURT
44	341	17.6	892	1	AL525099	AL525099
45	337.5	17.4	898	4	BI819396	603034571

ALIGNMENTS

RESULT 1	AK076364	4439 bp	mena	linear	HTC 03-APR-2004
LOCUS	Mus musculus	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732468D08	product:P2Y4 RECEPTOR, full insert sequence.		
DEFINITION	AK076364				
ACCESSION	AK076364.1	GI:26345325			
VERSION	AK076364.1				
KEYWORDS	HTC; CAP trapper				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,				

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE20530913
PUBMED11076861
REFERENCE4
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

JOURNAL
REFERENCE

Nature 409, 685-690 (2001)

5
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

JOURNAL
REFERENCE

Nature 420, 563-573 (2002)

6
AUTHORS

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4439)
Adachi, J., Aizawa, K., Akimura, T., Azakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, I.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, I., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.

JOURNAL
REFERENCE

Submitted (16-APR-2002)

Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.Location/Qualifiers
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match=1083)
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source

CD5

ORIGIN

Alignment Scores:

Pred. No.: 3,596-33 Length: 4439
Score: 460.50 Matches: 121
Percent Similarity: 49.71% Conservative: 49
Best Local Similarity: 35.38% Mismatches: 125
Query Match: 23.78% Indels: 48
DB: 3 Gaps: 8

US-10-763-972-2 (1-360) x AK076364 (1-4439)

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QY 57 AlaTyrSerIlellePheleLeuGlyLeuProLeuAenGlyThrValLeuPheSer 76
DB 407 AGCTATGAGATGTCTTTGTGTGGGCTGGCCCTCAATGCCCAACCTTTGGCTGTC 466

QY 77 TrpGlyGlnThrLysArgTyrSerCysAlaThrThrTyrLeuValAsnLeuMetValAla 96
DB 467 CTCTTCCGCTTCGGACCTGGGATGCAACAGCCCTTACATGTTCCATTTGGCAATTGCA 526

QY 97 AspLeuLeuTyrValLeu---LeuProPheLeuIlelleThrTyrSerLeuAspArg 115
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QY 116 TrpProPheGlyGluLeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyr 135
DB 587 TGCGCCTTTGGCAGCTGCTTCTGCAAGTCTGCGCTTCTTTCTACTGGAACCTCTAC 646

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QY 156 LeuCysSerLeuProTyrArgThrArgHisAlaTrpLeuGlyThrSerThrTyrTrp 175
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QY 235 PheThrAspGlyGlnGluProAspGlnAlaArgGlyGluProHisGluAspArgGlnHis 254
DB 946 TGGACT-----CAT 954

QY 255 SerProSerGlnVal----- 259
DB 955 GGCCCGGCGACTGTATCGAOCCTTTGCCAGGAGCTGGACAGTCATCTTCTCGGCTCCGCTTC 1014

QY 260 HisProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyr 279
DB 1015 TCTCGCACCATCTGCTGTGGTGTGCTGCTTTTGTGCTGTCTGCTGCTTGTCCACAT 1074

QY 280 HisSerLeuLeuLeuProHisHisLeuLeu-----SerAlaPheSerGlyLeuPro 296
DB 1075 CAC-----CGGCAACATTTATTACCTGGCAAGACTGTTGAACGCCGCAATCCG 1122

QY 297 AlaLeuAspGlySerGlnCysGlyLeuGlnAspMetGluAserGlyGluCysGluGln 316
DB 1123 GGTCTGAACATTGCTCAATGTGGTTTCAAGTAGCTGCTCCCTGGCCAGTCTAATAG 1182

QY 317 LeuProGlnProSerProValLeuSer-PheLysGlyGlyLysAsnArgValArgLeuLe 336

D	b		127	CTACTGGGGCGTCCCACTCAATGCCGTGTGTCATTGGGCAGATCTGGCTGGCCCGGAAGCGC	186
Q	y		83	TpSerCysAlaThrThrTyLeuValAsnLeuMetValAlaAspLeuLeuTyValLeu	102
D	b		187	TTGACCGCCACCACCATCTACATCTGAACCTGGCCATGGCCGACGCTGTTATGTCTGCG	246
Q	y		103	--LeuProPheLeullelleThrTySerLeuAspArgTrpProPheGlyGluLeu	121
D	b		247	TCCCTCCCTCTCCATCTACACTACACCAGAAGATTACTGGCCCTTTGGGACATTC	306
Q	y		122	LeuCysLysLeuValHisPheLeuPheTyTlleAasnLeuTyGlySerIleLeuLeuLeu	141
D	b		307	ACCTGCATAATCGTGCCGCTTCCAGTTCTTACACCAACCTGCACGGCAGATCCTCTTCCTC	366
Q	y		142	ThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCySerLeu--Pro	160
D	b		367	ACCTGCATCACGTCACGCTCATATGGGATCTGCCACCCCTTGGCCTCGTGGGCACAA	426
Q	y		161	TyArgThrArgArgHisAlaTrpLeuglyThrSerThrThrTrpAlaLeuValValLeu	180
D	b		427	AAGAAGGANAAGAGCTGACGTGGTGTGTGTGCTGGCTGCTGCTATCATCTCATCGCC	486
Q	y		181	GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyTlleAasnGlyGlnMetIleTrp	200
D	b		487	CAGTGCCTCGCCACCTTTGCTTGGCTCCACCGGCACGACGAGNAATCGCATCTGTCTGC	546
Q	y		201	TyrAspMetThrSerGlnGlnAasnPheAspArgLeuPheAlaTyrglyIleValLeuThr	220
D	b		547	TATGACCTGAGCCCCCGGACCGCTCCACATCTACTTCCCCTATGGCATCACGTTGACC	606
Q	y		221	LeuSerGlyPheLeu--SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG	240
D	b		607	ATACCGGCTTCTGCTGCCCTTCGACGCATCTCGCTGCTACTGCAGCATGGCCCGC	666
Q	y		240	lupro 241	
D	b		667	ATCCT 671	
RESULT	3				
AY400799					
LOCUS			987 bp	DNA linear	GSS 15-DEC-2000
DEFINITION			Mus musculus P2RY6 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION			AY400799		
VERSION			AY400799.1	GI:39756788	
KEYWORDS			GSS.		
SOURCE			Mus musculus (house mouse)		
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,		
			Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,		
			Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
			Adams,M.D. and Cargill,M.		
TITLE			Infering nonneutral evolution from human-chimp-mouse orthologous		
JOURNAL			Gene trios		
PUBLISHED			Science 302 (5652), 1960-1963 (2003)		
REFERENCE			14671302		
AUTHORS			2 (bases 1 to 987)		
			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,		
			Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,		
			Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
			Adams,M.D. and Cargill,M.		
TITLE			Direct Submission		
JOURNAL			Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		
			Rockville, MD 20850, USA		
COMMENT			This sequence was made by sequencing genomic exons and ordering		
			them based on alignment.		
FEATURES			Location/Qualifiers		
source			1..987		
			/organism="Mus musculus"		
			/mol type="genomic DNA"		

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ORIGIN
Alignment Scores:
Pred. No.: 2,97e-30 Length: 987
Score: 420.50 Matches: 117
Percent Similarity: 45.05% Conservative: 47
Best Local Similarity: 32.14% Mismatches: 125
Query Match: 21.72% Indels: 76
DB: 9 Gaps: 9

US-10-763-972-2 (1-360) x AY400799 (1-987)

QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeu-----CysGln 44
DB 1 ATGGAGCAG--GACATGGCACCATCCAGGCTCCAGGCTTCGCGCCACCACTGGCTC 57
QY 45 PheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheLeu 64
DB 58 TACCGTGAGGATTTCAAGCGACTCTCTGTAACCCGATATCTCGGTGGTGGTCTG 117
QY 65 GlyLeuProLeuAsnGlyThrValLeuThrHisSerTrpGlyGlnThrLysArgTrpSer 84
DB 118 GGCTGGCCACTGACATCTGGCTGATGGCCAGATCTGGCATCCGCGGACCTTGACC 177
QY 85 CysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---Leu 103
DB 178 CGTTCCGCTGTGTACACCTGACCTGGCACTGGCGGACCTGATGTATGCTGTCTACTA 237
QY 104 ProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCys 123
DB 238 CCCCTACTTACTAATACGACGAGGAGGACCACTGGCCCTTCGGAGACTCGCGCTGC 297
QY 124 LysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuThrCys 143
DB 298 CGCTTTGTACGCTTCTCTTCTATATGCAATCTACATGGCAGCATCTGTTCTCTCACTGC 357
QY 144 IleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg--- 162
DB 358 ATTAGCTTCACGCGCTACCTGGGATCTGCCATCTGCCACCCCTGCTTCCTGGCACAAGCTGGA 417
QY 163 ThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuLeu 182
DB 418 GGTGCGCTGCTGCTGGTAGTGTGGAGTGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 477
QY 183 LeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAsp 202
DB 478 CTGCCCCACGACGCTTTGTGTGTCACAGGATCCAGCGCAACGCGCATGTGTGTGTGTGTGTGTGTGT 537
QY 203 MetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSer 222
DB 538 CTGAGCCCCATCCTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 597
QY 223 GlyPheLeu--SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProA 242
DB 598 GGCTTCTTGTGCGCTTCATAGCCTTACTGGCTTGTATTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 641
QY 242 spGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHisProA 262
DB 642 -----CATGCCCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
QY 262 sphIsProThr----- 265
DB 667 GATGGCCCCAGCGTCTGTGGCCCAAGACGCGCGCAGCAAGCGGCTCGTATGTGTGTGTGTGTGTGTGTGT 726
QY 266 -----GlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeu 284
DB 727 GTGGTGCACTGTCTTGTGCACTCAGCTT---CCTGCTTTTCCATCATCACCAGACGCG 783
QY 284 euProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysG 304

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DB 784 TACTTGGCTGTGCTCCAGCGGCTGTCTTCCCTGTGCTGGAGACCTTCCGCTGCT 843
QY 304 LysLeuGlnAspMetGluAlaSerGlyGluCysGluGln----- 316
DB 844 GCCTACAAAGGCACCTCGGCCCTTCGCCAGTGTCAACAGTGTCTCGGACCCCATCTCTCTTC 903
QY 317 -----LeuProGlnProSerProValLeuSerPheLysGlyGlyLysA 331
DB 904 TACTTCAACACACAGAGTTCGGGGGCAACCCCAAGATCTCTTACAGAGGCTCACAG- 961
QY 331 snArgValArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyGluHisProAlaGlyA 351
DB 962 -----CCAAAGTGGA 971
QY 351 fGlyArg 353
DB 972 GAGGCAGA 979

RESULT 4
AY400798 987 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes P2RY6 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY400798
VERSION AY400798.1 GI:39756787
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 987)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
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/mol_type="genomic DNA"
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gene

ORIGIN
Alignment Scores:
Pred. No.: 8.2e-30 Length: 987
Score: 416.00 Matches: 115
Percent Similarity: 47.59% Conservative: 33
Best Local Similarity: 36.98% Mismatches: 128
Query Match: 21.49% Indels: 36
DB: 9 Gaps: 10

US-10-763-972-2 (1-360) x AY400798 (1-987)

QY 33 AspMetAsnThrSerGlnGlnGlyLeu-----CysGlnPheSerGluLys 48
DB 10 GACAAATGGCAGCGCCAGGCTGTGGGCTTCCACCCACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 69

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QY	49	TyrlvsGlnValTyrlLeuSerLeuAlaTyrSerIleilePheileuGlyLeuProLeu	68
DB	70	TTCAAGCAACTGCTGCTGCACCTGTATTCGGCGGTGCTGGCGCTGCCGCTGCGCTG	129
QY	69	IenGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr	88
DB	130	RACACTCTGTGCATTACCAGATCTGCAGCTCCGCGCGGCGCTGACCCGCGCACGCCCGTG	189
QY	89	TyrlLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeuIle	107
DB	190	TACACCTTAACCTTGCTCTGGCTGACCTGCTATATGCTGCTGCTCCCTGCCCTGCTCATC	249
QY	108	IleThrTyrlSerLeuAspAspArgTrpProPheGlyGlnLeuLeuCysLysLeuValHis	127
DB	250	TACAACCTATGCCAAGGTGATCACTGGCCCTTTGGGAGCTTCGCCCTGCCGCTGCTGCCG	309
QY	128	PheLeuPheTyrlIleAsnLeuTyrlGlySerIleLeuLeuLeuThrCysIleSerValHis	147
DB	310	TTCTCTCTTATNGCCAACCTGCATGGCAGCATCTCTCTCTACCTGCATCAGCTTCAG	369
QY	148	GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHisHis	166
DB	370	CGCTACCTGGGCATCTGCACCCGCTGGCGCCCTGGCACAAAGTGGGGCGCGCGGGCT	429
QY	167	AlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeuLeuProThrLeu	186
DB	430	GCTGGCTAGTGTGTGTAGCCGTGTGCTGGCGGTGACACCCAGTGCCTGCCCAAGCC	489
QY	187	AlaPheSerHisThrAspTyrlIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln	206
DB	490	ATCTTTGCTGCCACAGGCATCCAGCGTAACCGCACTGCTGTATGACCTCAGCCGCGCT	549
QY	207	GluAsnPheAspArgLeuPheAlaTyrlGlyIleValLeuThrLeuSerGlyPheLeu---	225
DB	550	GCCCTGGCCACCACCATATATCCCTACGGCATGGCTCTCACTGCATCGGCTTCCTGCG	609
QY	226	-----SerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAsp	242
DB	610	CCCTTGTGCTGCTGCTGGCTGCTACTGTCTCTG-----	645
QY	243	GlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAsp	262
DB	646	----GCCCG------CGCTGTGCGCGCAGATGCGCCGCGCAGAG-----CCTGT-	686
QY	263	HisProThrGlyValTrpProLeuHisPro-----LeuPheCys	275
DB	687	GGCCCCAGGCGCGGTGGCAAGGCGGCCCGCATGCGCGTGGTGGTGGCTGCTTTTGC	746
QY	276	---AlaLeuPro-----TyrlHisSerLeuLeuLeuProHisHisLeuLeuSerAla	291
DB	747	CATCAGCTTCTTACCTTTTTCATCATCACCAAGACAGCCTACCTGGCAGTGGCTCAACGCC	806
QY	292	PheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMetGluAlaSer	311
DB	807	GGCGGTCCTGCATGTATTGGAGGCGCTTTGAGCGCGCTTACAAAGGCACGCGCGCTT	866
QY	312	GlyGlyCysGluGlnLeuProGlnProSerPro	322
DB	867	TGCAGTGCACACAGCGTCTGGACCCCATCCN	899
RESULT 5			
LOCUS	CR624871	1425 bp	mRNA linear HTC 21-JUL-2000
DEFINITION			full-length cDNA clone CS0D1035Y19 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION	CF624871		
VERSION	CR624871.1	GI:50505678	
KEYWORDS	HTC; CDSLT_CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue

2 (bases 1 to 1425)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN
Alignment Scores:
Pred. No.: 2,02e-29 Length: 1425
Score: 414.50 Matches: 133
Percent Similarity: 43.29% Conservative: 38
Best Local Similarity: 33.67% Mismatches: 166
Query Match: 21.41% Indels: 60
DB: 3 Gaps: 10

US-10-763-972-2 (1-360) x CR624871 (1-1425)

Qy 8 SerArglySerArgSerGlySerArgArgGlyAlaLeuLeuGluGlyAlaSerArg 27
::: ||||| :::
Db 45 GCTGAGGGCAGGAGATGGGGAGGCTCAGGTCTGGCTTCCTTTGCCCAACACACTGG 104
::: ||||| :::
Qy 28 AspMetGluLysVal----- 32
::: ||||| :::
Db 105 GACCACCGCGTGCTGCAGGACACGAGGCGTCCCTCCTGAACATAGGAACCCACC 164
::: ||||| :::
Qy 33 -----AspMetAsnThrSerGlnGlnGlyLeu----- 42
::: ||||| :::
Db 165 TGGCGACCCATGGAATGGACAATGGCACAGGCCAGGCTCTGGGCTGCCACCCACCACC 224
::: ||||| :::
Qy 43 CysGlnPheSerGluLysTyrltyrGlnValTyrLeuSerLeuAlaTyrSerlleilephe 62
::: ||||| :::
Db 225 TGTTCTACCGCGAGAATTCAAGCAAATGTGCTGCCACCTGTGTATTCGGCGGTGTG 284
::: ||||| :::
Qy 63 IleLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArg 82
::: ||||| :::
Db 285 CGCGCTGGCGCTCCGCTGAACATCTGTGTCAATCCCAGATCTGCACGTCCTCCCGCGGCC 344
::: ||||| :::
Qy 83 TrpSerCysAlaThrTyrTyrLeuValasnLeuMetValAlaAspLeuLeuTyrValleu 102
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Db 345 CTGACCCGCGACGGCGGTGTACACCTAAACCTTGGCTGGGTACCTGCTATATGCCGTGC 404
::: ||||| :::
Qy 103 ---LeuProPheLeullelleThrTyrSerLeuAspAspArgTrpPropheGlycylleu 121
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Db 405 TCCTGTGCCCTCGCTCATCTACAACTATGCCAAGGTGNCTACTGGCCCTTTGGGACTTC 464
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Qy 122 LeuCystlysLeuValHisPheLeuPheTyrilleAsnLeuTyrGlySerlleileuLeu 141
::: ||||| :::
Db 465 GCCTGCGCGCTGGTCGGCTTCTCTTCTATGCCAACCTGCACGGCAGCATCTCTTCCTC 524
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Qy 142 ThrCyslleSerValHisGlnPheLeuclylValCysHisProLeuCysSerLeuProTyr 161
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/notes="unnamed protein product; PURINERGIC RECEPTOR P2Y,
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VIMARLLRPAYTGTGLPRKRSVRTIALVFAUCFLPFLHTRITRILYISFRSLDL
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ORIGIN

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Alignment Scores:
Pred. No.: 4.88e-29 Length: 2542
Score: 414.50 Matches: 132
Percent Similarity: 48.66% Conservative: 50
Best Local Similarity: 35.29% Mismatches: 155
Query Match: 21.41% Indels: 38
DB: 3 Gaps: 9

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US-10-763-972-2 (1-360) x AK017378 (1-2542)

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Qy 2 LeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgArgGlyAlaLeuLeu 21
Db 435 CTGAGCATCTC-----ACCACCTCAAGACGAGGAGTGATCAG 473

Qy 22 LeuGluGly-AlaSerArgAspMetGluLysValAspMetAsnThrSer----- 37
Db 474 GTCCAGGGCAATGCGACGACCTGGAACCTCGAATAGCACCATCAATGGACCTGGGA 533

Qy 38 ----GlnGluGlnGlyLeu---CysGlnPheSerGluLysTyrsLysGlnValTyLeuSe 55
Db 534 GGGGACCAACTGGATCAAGTGTCTGTTTCAACGAGGACTTCAAGTACGTGTGTGCC 593

Qy 55 rLeuAlaTyrsIlelePheIleLeuLeuGlyLeuProLeuAsnGlyThrValLeuTrpHi 75
Db 594 CGTGCTCTAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 653

Qy 75 sSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThrTyrsValAsnLeuMetVa 95
Db 654 CTCTCTATGCGGCTCAAAACCTGGAACGCTCCACCATCATGTTCACCTGGCAGT 713

Qy 95 lAlaAspLeuLeuTyrrValLeu---LeuProPheLeuIleIleThrTyrsSerLeuAspAs 114
Db 714 TTCGACTCTCTACGACGCTCCCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 773

Qy 114 pArgTrpPheGlyGluLeuLeuCysLysLeuValHisPheLeuPheTyrrIleAsnLe 134
Db 774 CCACTGGCCATTAGCAGCGTGTCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 833

Qy 134 uTyrrGlySerIleLeuLeuLeuThrCysIleSerValHisGlnPheLeuGlyValCysHi 154
Db 834 CTACTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 893

Qy 154 sProLeuCysSerLeuProTyrrArgThrArgArgHisAlaTrpLeuGlyThrSerThrTh 174
Db 894 CCCTCTGCACTCCCTGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGT 953

Qy 174 rTrpAlaLeuValValLeuGlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrril 194
Db 954 GTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1013

Qy 194 eAsnGlyGlnMetIleTrpTyrrAspMetThrSerGlnGluAsnPheAspArgLeuPheAl 214
Db 1014 GGGAAACCGGATCACTTGGCCATGACACCTCGGCCGAGAGAGCTCTTTAGCCATTTTGGGC 1073

Qy 214 aTyrrGlyIleValLeuThrLeuSerGlyPhe---LeuSerLeuLeuGlyHisPheGlyVa 233
Db 1074 TTACAGCTCCGTCATGTGTGGG-TCTGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1132

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Qy 233 lLeuPheThrAspGlyGlnGluProAspGlnAlaArgGlyGluProHisGluAspArgGl 253
Db 1133 GTTACGTGCTTATGCCAGGGGGCTGCTCAACCGGCTTATGGACCAAGGAGTGTGC 1192

Qy 253 nHisSerProSerGlnValHisProAspHisProThrGlyValTrpProLeuHisProLe 273
Db 1193 CTCGGGCAAGCGAAGTCTGTGGCCACCATTCGCTTGGTACTGGCCGCTCTTCGCCCTCT 1252

Qy 273 uPheCysAlaLeuProTyrrHisSer-----LeuLeuLeuProHisHisLeuLeuSe 290
Db 1253 GCTTCTGCTTCTTCACTCAGCGGACCCCTCTACTACTCTCTCTCG-----AT 1300

Qy 290 rAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMetGluAl 310
Db 1301 CACTTGACCTCAGCTGCGCACACCTCAACGCGCATCAACATGGCATTAAGATCAACCCGCG 1360

Qy 310 aSerGlyCysGlnGlnLeuProGlnPro-SerProValLeuSerPheLysGlyGlyL 330
Db 1361 CGTGTGGCCAGCGCCCAACAGTTG-----TCTTGACCGGCTACTTCTTCTTCTGCGAGGGC 1414

Qy 330 ysAsnArgValArgLeuLeuGlnLysLeuArg----- 340
Db 1415 AGAGACTTGTTCGGTTCGCGGAGATGCCAAGCCACCCAGGAGCTACCCGACGCCAC 1474

Qy 341 ----GlnAsnLysLeuGlyGluHisProAlaGlyArg 351
Db 1475 AGGCTCGTGGCAAGTGGGCTGCACAGGCGCTAACAAGA 1512

RESULT 7
AK005013 3001 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male liver cDNA, RIKEN full-length enriched
DEFINITION library, clone:130001504 product:PURINERGIC RECEPTOR P2Y,
G-PROTEIN COUPLED 2, full insert sequence.
ACCESSION AK005013
VERSION AK005013.2 GI:26339698
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishise, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Nature 409, 685-690 (2001)
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3001)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
On Dec 10, 2002 this sequence version replaced gi:12836638.
Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGCGCACTCGAGTCTTTTATTTTNN 3'], cDNA was prepared by using triazole thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGATCAGAGCTCAATTAATTAACCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
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ORIGIN
Alignment Scores:
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Score: 414.50 Matches: 132
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Best Local Similarity: 35.29% Mismatches: 155
Query Match: 21.41% Indels: 38
DB: 3 Gaps: 9
US-10-763-972-2 (1-360) x AK005013 (1-3001)
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QY 22 LeuGluGly-AlaSerArgAspMetGluLysValAspMetAsnThrSer----- 37
DB 467 GTCCAGGCAATGCCAGCAGCAGCTGAGACCTGGATAGCACCATCAATGGCAGCTGGGA 526
QY 38 -----GlnGluGlnGlyLeu---CysGlnPheSerGluLysTyrLysGlnValTyrLeuSe 55
DB 527 GGGGACGAACCTGGGATACAAAGTGTGCTTCAACGAGGACTTCAAGTACGTGCTGTTGCC 586
QY 55 rLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrPHe 75
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QY 75 sSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetVa 95
DB 647 CTTCTATGCGCCCTCAAAACCTGCAACCCCTCCACACCTACATGTTTTCACCTGGCAGT 706
QY 95 lAlaAspLeuLeuTyrValLeu---LeuProPheIleIleIleThrTyrSerLeuAspAs 114
DB 707 TTGGGACTCTCTTACGAGCGCTCCCTCCGCTGTGTTATTACTACGCCCGGGGTGA 766
QY 114 pArgTrpProPheGlyGluLeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLe 134
DB 767 CCACTGGCCATTTAGCACGGTGCTCTGCAAGCTGGTGGTTTCTCTTCTACACCAACCT 826
QY 134 uTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGlnPheLeuGlyValCysHi 154
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DB 1007 GGGAAACCGGATCACTTGCCATGACACCTCGCGCCGAGAGCTCTTTAGCCATTTTGGGC 1066
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QY 253 nHisSerProSerGlnValHisProAspHisProThrGlyValTrpProLeuHisProLe 273
DB 1186 CTCGGGCAACGCGAAGTCTGTGGCAGCAGTTCCTTGGTGGTACTGGCGCTCTTCCCTCT 1245
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 1515)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1515)
DB

REFERENCE
1 (bases 1 to 1515)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1044YA15"
/issue_type="Placenta Cot 25-normalized"
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ORIGIN

Alignment Scores:
Pred. No.: 4.87e-29 Length: 1515
Score: 411.00 Matches: 126
Percent Similarity: 45.85% Conservative: 34
Best local Similarity: 36.10% Mismatches: 152
Query Match: 21.23% Indels: 39
DB: 3 Gaps: 9

US-10-763-972-2 (1-360) x CR612681 (1-1515)

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QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIlePheLeuGlyLeuProLeu 68
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QY 69 AsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThr 88
DB 391 AACATCTGTCTATTACCCAGATCTGCACGTCCTCCGCGCGCCCTGACCCGCGCGTG 450
QY 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeu 107
DB 451 TACACCTAACCTTGCTGTGGCTGACCTCTATATGCTGCTCCCTGCCCTGCTCATC 510
QY 108 IleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCysLysLeuValHis 127
DB 511 TACAACATATGCCAAGGTATCACTGGCCCTTTGGCGACTTGGCCTGCTGCTGCTCG 570
QY 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
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QY 148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHis 166
DB 631 CGTACTCTGGCATCTGCCACCCGCTGGCCCTGGCCACCAAGCTGGGGCGCGCGGCT 690
QY 167 AlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeuLeuProThrLeu 186
DB 691 GCTGTGCTAGTGTGTAGCGGTGTGGCTGGCGGTGACCAACCAAGCTGCTGCCACAGCC 750
QY 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln 206

DB 751 ATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTGTATGACCTCAGCCGCGCT 810
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QY 246 lyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThr 266
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LOCUS
DEFINITION
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of Homo sapiens (human).
ACCESSION
CR618945
VERSION
CR618945.1 GI:50499752
KEYWORDS
HTC; CNSLT; cDNA.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1532)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1532)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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/organism="Homo sapiens"
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FEATURES
source


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RESULT 12

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DEFINITION of Homo sapiens (human).
ACCESSION CR626754
VERSION CR626754.1 GI:50507616
KEYWORDS HTC; CNSLT_cDNA;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1589)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1589)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-cligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/clone="CSODI024YE14"
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/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 5,246-29 Length: 1589
Score: 411.00 Matches: 126
Percent Similarity: 45.85% Conservative: 34
Best Local Similarity: 36.10% Mismatches: 152
Query Match: 21.23% Indels: 39
DB: 3 Gaps: 9
US-10-763-972-2 (1-360) x CR626754 (1-1589)

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QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
Db 401 TTCAGCAACTGCTGCTGCCACCTGTGTATTCGGCGGTGCTGGCGGCTGCGCTG 460
QY 69 AsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
Db 461 AACATCTGTGCTATACCCAGATCTGCCAGTCCCGCGCGCTGACCCGCGCAGCGCTG 520
QY 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeuIle 107
Db 521 TACACCTTAACCTTGCTGCTGCTGACCTGCTATATGCTGCTGCTGCTGCTGCTCATC 580
QY 108 IleThrTyrSerLeuAspArgTyrProPheGlyLeuLeuLeuCysLysLeuValHis 127
Db 581 TACAACCTATGCCAAGGTGATCACTGCGCCCTTTGGCAGACTTCGCGCTGCGCTGCGC 640
QY 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuTyrCysIleSerValHis 147
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QY 148 GlnPheLeuGlyValCysHisProLeuLeuCysSerLeuProTyrArg---ThrArgArgHis 166
Db 701 CGCTACCTGGCATCTGCCACCCGCTGGCCCTGGCCACAACTGGGGGCGCGCGCT 760
QY 167 AlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeuLeuProThrLeu 186
Db 761 GCCTGGCTAGTGTGTAGCGGTGTGGCTGGCTGACCAACCCAGTGCCTGCCACAGCC 820
QY 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrPyrAspMetThrSerGln 206

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Db      881 GCCTGGCCACCACTATATGCCATATGATGATGATGATGATGATGATGATGATGATG 940
Qy      226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgG 246
Db      941 CCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 997
Qy      246 lylGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrG 266
Db      998 GATGGCCC-----GCCAGAGCTGTGGCCAGAGCGGCTGGCAAGCGGCCCGCATG 1051
Qy      266 lylValTrp-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
Db      1052 GCCG-TGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy      282 LeuLeuLeuProHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
Db      1108 GACAGCTACTCTGGCAGTGGCTGCGAGCGCGGCGTCCCTGACACTGATGATGAGGCTT 1167
Qy      302 GlnCysGlyLeuGlnAspMetGluAlaSerGlyGlyCysGlnGluProGlnProSer 321
Db      1168 TGCAGGGCTCTACAAAGGCACGGCGGCTTGGCAGTGGCCACAGCGCTGTGACCCCAT 1227
Qy      322 ProValLeuSerPheGlyGlyGlyLysAsnArgValArgLeuLeuGlnLysLeuArgGln 341
Db      1228 CCT-----CTTCTACT-TCACCCAGAGA 1250
Qy      342 AsnLysLeuGlyGluHis-----ProAlaGlyArgLysArg 353
Db      1251 AGTTCGCGCGGACACATGAGCTCTCTACAGAACTCAGAGCAATGCGAGGCGAGG 1310
Qy      354 CysProGlyLeuAsnArgSer 360
Db      1311 GTGCTGAGTCTCCAGGTCC 1331

RESULT 13
LOCUS   CR605588
DEFINITION full-length cDNA clone CS0DI040YB02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR605588
VERSION   CR605588.1 GI:50486395
KEYWORDS  HTC; CNSLT cDNA.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1592)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
REMARK    Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1592)
REFERENCE 2 (bases 1 to 1592)
AUTHORS   Genoscope.
TITLE      Direct Submission
JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
     1..1592
         /organism="Homo sapiens"
         /mol_type="mRNA"

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/db xref="taxon:9606"
/clone="CS0DI040YB02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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ORIGIN

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Alignment Scores:
Pred. No.: 5,26e-29 Length: 1592
Score: 411.00 Matches: 126
Percent Similarity: 45.85% Conservative: 34
Best Local Similarity: 36.10% Mismatches: 152
Query Match: 21.23% Indels: 39
DB: 3 Gaps: 9

US-10-763-972-2 (1-360) x CR605588 (1-1592)
Qy      33 AspMetAsnThrSerGlnGlnGlnGlyLeu-----CysGlnPheSerGlyLys 48
Db      349 GACAAATGGCACAGCCAGGCTCTGGGCTTGCCACCCACCTGTCTACCGCGAGAAC 408
Qy      49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheIleLeuGlyLeuProLeu 68
Db      409 TTCAGCAACTGCTGCTGCCACCTGTGATTTCGGCGGTGCTGGCGTGGCTCCCGCTG 468
Qy      69 AsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
Db      469 AACATCTGTGTCTATTACCCAGATCTGCACGTCCGCGCGCCCTGCACCCGACGCGCGTG 528
Qy      89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeuIle 107
Db      529 TACACCTTAACCTTGTCTGCTGACCTGTATATGCTGCTCCCTGCTCCCTGCTCATC 588
Qy      108 IleThrTrpSerLeuAspAspArgTrpProPheGlyGluLeuLeuCysLysLeuValHis 127
Db      589 TACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTTGGCTGCGCTGCTCCGCT 648
Qy      128 PheLeuPheTyrIleAsnLeuTyrClySerIleLeuLeuLeuThrCysIleSerValHis 147
Db      649 TTCCTCTTCTATATGCCAACCTGCAGCGGAGCATCTCTTCTCCTACCTGATCAGCTTCAG 708
Qy      148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgArgHis 166
Db      709 CGCTACTCTGGGATCTGCCACCCGCTGGCCCTGGCACAAACGTGGGGCGCGCGGCT 768
Qy      167 AlaTrpLeuGlyThrSerThrTrpAlaLeuValLeuGlnLeuLeuProThrLeu 186
Db      769 GCCTGGCTAGTGTGTAGCCGTGTGGTGGCGGTGACAAACCCAGTGGCTGCCACAGCC 828
Qy      187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln 206
Db      829 ATCTTGGCTGCCACAGGATCCAGCGTAACCGCACTGTCTGCTAGCTCAGCCCGCT 888
Qy      207 GluAsnPhaAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
Db      889 GCCTGGCCACCACTATATGCCCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
Qy      226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgG 246
Db      949 CCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1005
Qy      246 lylGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrG 266
Db      1006 GATGGCCC-----GCCAGAGCTGTGGCCAGGAGCGCGGTGGCAAGCGGCCCGCATG 1059
Qy      266 lylValTrp-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
Db      1060 GCCG-TGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
Qy      282 LeuLeuLeuProHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
Db      1116 GACAGCTTACCTGGCAGTGGCTCGACGCGCGGCGCTCCCTGCACTGTATTGAGGCTT 1175
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RESULT 14
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DEFINITION
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25-normalized of Homo sapiens (human).
ACCESSION
CR606834
VERSION
1
GI:50487641
KEYWORDS
HTC; CNSUT_cDNA.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1594)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1594)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segres@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1594
/organism="Homo sapiens"
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/clone="CS0DC014YB07"
/tissue_type="Neuroblastoma Cot 25-normalized"
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ORIGIN
Alignment Scores:
Pred. No.: 5,27e-29 Length: 1594
Score: 411.00 Matches: 126
Percent Similarity: 45.85% Conservative: 34
Best Local Similarity: 36.10% Mismatches: 152
Query Match: 21.23% Indels: 39
DB: Gaps: 9

US-10-763-972-2 (1-360) x CR606834 (1-1594)

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Qy      49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerIlePheIleLeuGlyLeuProLeu 68
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Qy      69 AsnGlyThrValLeuTrpHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
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Qy      108 IleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCysLysLeuValHis 127
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Qy      128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
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Qy      148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgArgHis 166
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Qy      167 AlaTyrLeuGlyThrSerThrTrpAlaLeuValLeuGlnLeuLeuProThrLeu 186
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Qy      187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyrTyrAspMetThrSerGln 206
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Qy      207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
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Db      870 GCCCTGGCCACCCACTATATGCCATGCTATGCGATGGCTCTCACTGTCTGCTGCTG 929
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Qy      226 exLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlnProAspGlnAlaArg 246
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Db      930 CCTTTGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
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Qy      246 IyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrG 266
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Qy      266 IyValTrp-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
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Db      1041 GCGG-TGGTGGTGGCTGCTGCTTTGGCCATCAGCTT---CCTGCTTTTTCATCACCACAA 1096
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Qy      282 LeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySer 301
               |||||
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of Homo sapiens (human).
ACCESSION
CR617080
VERSION
1
GI:50497887
KEYWORDS
HTC; CNSUT_cDNA.
SOURCE
Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1638)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1638)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
JOURNAL
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
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Alignment Scores:
Pred. No.: 5,49e-29 Length: 1638
Score: 411.00 Matches: 126
Percent Similarity: 45.85% Conservative: 34
Best Local Similarity: 36.10% Mismatches: 152
Query Match: 21.23% Indels: 39
DB: 3 Gaps: 9
US-10-763-972-2 (1-360) x CR617080 (1-1638)
QY 33 AspMetAsnThrSerGlnGluGlnGlyLeu-----CysGlnPheSerGluLys 48
Db 374 GACAATGGCAGCCAGGCTCTGGGCTTCCACCCACACCTGTGTCTACCCGAGAAC 433
QY 49 TyrlsGlnValTyrLeuSerLeuAlaTyrSerIlePheIleLeuGlyLeuProLeu 68
Db 434 TTCAAGCACTGCTGCTGCCACCTGTGTATTGGGGTGTGGCGGTGGCTGGCGCTG 493
QY 69 AsnGlyThrValLeuThrHisSerTrpGlyGlnThrLysArgTrpSerCysAlaThrThr 88
Db 494 AACATCTGTGTGATACCCAGATCTGCACGTCCCGCGGCCCTGACCCGCGCGGTG 553
QY 89 TyrLeuValAsnLeuMetValAlaAspLeuTyrValLeu---LeuProPheLeuIle 107
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QY 108 IleThrTyrSerLeuAspArgTrpProPheGlyGluLeuLeuCysLysLeuValHis 127
Db 614 TACAACATATGCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCGCTGGCCCTGGTCCGC 673
QY 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuThrCysIleSerValHis 147
Db 674 TTCTCTTCTATGCAACCTGCGGAGCATCTCTTCCCTACCTGATCAGCTTCCAG 733
QY 148 GlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArg---ThrArgHis 166
Db 734 CGCTACCTGGGCATCTGCCACCCGCTGGCCCTGGCACAAACGTGGGGCGCGGGCT 793
QY 167 AlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeuGlnLeuLeuProThrLeu 186
Db 794 GCCTGGCTAGTGTGTAGCCGTGTGGCTGGCGGTGACAAACCCAGTGCCTGCCACAGCC 853

QY 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln 206
Db 854 ATCTTCGCTGCCACAGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCGCT 913
QY 207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeu--S 226
Db 914 GCCCTGGCCACCACTATATGCCCTATGGCATGGCTCTCACTGTATCGGCTTCTCTG 973
QY 226 erLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArg 246
Db 974 CCCTTGCTGCCGTGGCTGTACTGTCTCTGGCCTG---CCGCCTGTGCCGCGAG 1030
QY 246 lyGluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThr 266
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QY 266 lyValTrp-----ProLeu-HisProLeuPheCysAlaLeuProTyrHisSer 281
Db 1085 GCCG-TGTGTGGCTGTGCTTGGCTTGGCATCAGTT---CCTGCCTTTTACATCACAA 1140
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Db 1141 GACAGCCTTACCTGGCAGTGGCTCGACGCGGGGCTCCCTGCACTGTATTGGAGGCTT 1200
QY 302 GlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnProSer 321
Db 1201 TCGAGCGGCTTACAAAGCAGCGCGGCTTGGCAGTGCCACAGCGTGTGGACCCCAT 1260
QY 322 ProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeuArgGln 341
Db 1261 CCT-----CTTCTACT-TCACCCAGAAGA 1283
QY 342 AsnLysLeuGlyGluHis-----ProAlaGlyArgLysArg 353
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QY 354 CysProGlyLeuAsnArgSer 360
Db 1344 GTCGCTGAGTCTCTCCAGGTCC 1364

Search completed: November 10, 2004, 13:16:13
Job time : 3872 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 04:41:06 ; Search time 603 Seconds

(without alignments)
9419.359 Million cell updates/sec

Title: US-10-763-972-1

Perfect score: 1082

Sequence: 1 atgcgtccattttgttcc.....ccagggttgaaacagatctgg 1082

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1082	100.0	1156	10	Adb99257 Human p2Y
3	1082	100.0	1334	10	Adc86166 Human GPC
4	1082	100.0	3143	6	Aas17746 Human gen
5	1059	97.9	1108	6	Adi16623 Human NOV
6	1059	97.9	1108	12	Adn42283 Human CDN
7	1051	97.1	1063	6	Aas98135 Human DNA
8	1006	93.0	1017	10	Adc25999 Human pur
9	1006	93.0	1017	10	Adc25999 Human pur
10	1002.8	92.7	1020	6	Adb61648 Human GPC
11	1002.8	92.7	1076	6	Abq79300 Human GPC
12	1002.8	92.7	1076	6	Adc29667 Human G-p
13	996.4	92.1	1002	4	Ado30395 Human GPC
14	850	78.6	850	6	Aah73516 Human G p
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16	510	47.1	510	4	Ado30397 Mouse GPC
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19	370	34.2	585	4	Aas30774 Human CDN
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23	227.8	21.1	2025	6	ABZ35611	Abz35611 Human gen
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25	227.8	21.1	2025	10	ACA56884	Aca56884 Human sig
26	227.8	21.1	2025	12	ADI56680	Adi56680 Human pol
27	227.8	21.1	2025	12	ADP49188	Adp49188 Human p2Y
28	226.2	20.9	2118	6	ABZ35320	Abz35320 Human gen
29	224.6	20.8	2547	12	ADP21380	Adp21380 Gene P2RY
30	223.6	20.7	1163	4	AAD04981	Aad04981 Human pur
31	222	20.5	551	4	AAS42837	Aas42837 Human G p
32	202.2	18.7	1122	12	ADO30307	Ado30307 Mouse GPC
33	202.2	18.7	1842	2	AAQ88134	Aaq88134 Human P20
34	202.2	18.7	2138	6	AAZ32944	Aaz32944 Mus muscu
35	202.2	18.7	2138	6	AAZ32937	Aaz32937 Mus muscu
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38	178.6	16.5	1098	12	ADO30018	Ado30018 Human GPC
39	178.6	16.5	1428	12	ADP21381	Adp21381 Gene P2RY
40	178.6	16.5	1429	2	AAT74321	Aat74321 Human P2Y
41	178.6	16.5	1429	10	ACA56470	Aca56470 Human sig
42	178.6	16.5	1429	12	ADI56266	Adi56266 Human pol
43	178.6	16.5	1429	12	ADP49192	Adp49192 Human p2Y
44	173.8	16.1	1651	10	ADE40462	Ade40462 Human pyr
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ALIGNMENTS

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ID ABQ76000 standard; DNA; 1082 BP.

XX
AC ABQ76000;

XX
DT 17-OCT-2002 (first entry)

XX
DE Human GPCR designated PFI-020 encoding sequence.

XX
KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
KW disorder; PFI-020; gene; ds.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 1..1080

FT FT /*tag= a

FT FT /partial

FT FT /product= "GPCR designated PFI-020"

FT FT /note= "no stop codon given"

XX
PN EP1215214-A1.

XX
PD 19-JUN-2002.

XX
PF 04-DEC-2001; 2001EP-00310137.

XX
PR 18-DEC-2000; 2000GB-00030855.

XX
PR 17-JAN-2001; 2001GB-00001222.

XX
PA (PFIZ) PFIZER LTD.

XX
PA (PFIZ) PFIZER INC.

XX
PI Fidock MD;

XX
DR WPI; 2002-510798/55.

XX
DR P-PSDB; ABB98145.

XX
PT New polynucleotide encoding G protein-coupled receptor PFI-020, useful
PT e.g. for treating eating and sleeping disorders and for identifying
PT specific modulators.

PS Claim 1 (c); Page 11; 23pp; English.

XX The invention relates to an isolated polynucleotide encoding a novel polypeptide belonging to the class of proteins known as G-protein coupled receptors (GPCRs). The activity of proteins of the invention may be described as, antidepressant and neuroleptic. Polynucleotides of the invention are used for recombinant expression of the G-protein-coupled receptor (PFI-020) polypeptides, to create transgenic animals, as source of primers, probes, antisense sequences and ribozymes and in gene therapy. Therapeutic agents of the invention can be used to treat a wide range of disorders, particularly mood disorders, depression or arousal, especially eating and sleeping disorders. The current sequence represents a coding sequence for a human GPCR designated PFI-020

XX Sequence 1082 BP; 218 A; 318 C; 277 G; 269 T; 0 U; 0 Other;

Query Match 100.0%; Score 1082; DB 6; Length 1082;
Best Local Similarity 100.0%; Pred. No. 3.9e-285;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCTGTCCATTTTCTTCTTCCAGGGGAGCAGAGAGCGGAGCGTGTGAGCTCTG 60
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Db 61 CTCCTGAGGAGCGCTCCGGGACATGGAGAGGTGGACATGAATACATCACAGGAACAA 120
Qy 121 GGTCTCTGCCAGTTCTCAGAGAGTCAACAGAGTCTACCTTCCCTGGCCTACAGTATC 180
Db 121 GGTCTCTGCCAGTTCTCAGAGAGTCAACAGAGTCTACCTTCCCTGGCCTACAGTATC 180
Qy 181 ATCTTTATCTAGGCGCCACATAATGGCACTGTCTTGGCACTCCTGGGSCCAAC 240
Db 181 ATCTTTATCTAGGCGCCACATAATGGCACTGTCTTGGCACTCCTGGGSCCAAC 240
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Qy 301 GTGCTATGCGCTTCTCATCATCACTACTACTAGATGACAGAGTGGCCCTGCGGGAG 360
Db 301 GTGCTATGCGCTTCTCATCATCACTACTACTAGATGACAGAGTGGCCCTGCGGGAG 360
Qy 361 CTGCTCTGCAAGCTGTGGTGCATCTCTCTTATATCAACCTTTACGGCAGCATCTGCTG 420
Db 361 CTGCTCTGCAAGCTGTGGTGCATCTCTCTTATATCAACCTTTACGGCAGCATCTGCTG 420
Qy 421 CTGACCTGCAATCTGTGCAACAGTCTCTAGGTGTGTGCCACCATCTGTGCTGCC 480
Db 421 CTGACCTGCAATCTGTGCAACAGTCTCTAGGTGTGTGCCACCATCTGTGCTGCC 480
Qy 481 TACCGACCCGAGGATGCTGTGGGACACAGACACACCTGGGCGCTGTGGTCTTC 540
Db 481 TACCGACCCGAGGATGCTGTGGGACACAGACACACCTGGGCGCTGTGGTCTTC 540
Qy 541 CAGCTGTGCCCCACATGGGCTTCTCCACACCGGACTATCAATATGGCAGATGATCTGG 600
Db 541 CAGCTGTGCCCCACATGGGCTTCTCCACACCGGACTATCAATATGGCAGATGATCTGG 600
Qy 601 TATGACATGACAGGACCAAGATTTTGTGCGCTTTTGGCTTACGGCATAGTCTGACA 660
Db 601 TATGACATGACAGGACCAAGATTTTGTATCGCTTTTGGCTTACGGCATAGTCTGACA 660
Qy 661 TTGCTGCGCTTTCTTCCCTCTCTGCTGCTATTTGGTGTGCTATCTAGTGTGCTGAG 720
Db 661 TTGCTGCGCTTTCTTCCCTCTCTGCTGCTATTTGGTGTGCTATCTAGTGTGCTGAG 720
Qy 721 CCTGATACAGGACAGGACCACTCATGAGGACAGGACAGGACAGGACAGGACCAAT 780
Db 721 CCTGATACAGGACAGGACCACTCATGAGGACAGGACAGGACAGGACAGGACCAAT 780
Qy 781 CCGGACCATCTACTGTGTGTGTGGCTCTTCCACCTCTGTGCTGCTGCTTCCATATCAC 840

Db 781 CCGGACCATCTACTGTGTGTGTGGCTCTTCCACCTCTGTGCTGCTTCCATATCAC 840
Qy 841 TCGCTCTTCTTACCTTCCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGC 900
Db 841 TCGCTCTTCTTACCTTCCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGC 900
Qy 901 AGCAGTGTGCGCTTACAGATATGAGGCTCTGCTGAGTGTGAGAGCTGCTTCAACCC 960
Db 901 AGCAGTGTGCGCTTACAGATATGAGGCTCTGCTGAGTGTGAGAGCTGCTTCAACCC 960
Qy 961 AGTCTGTGCTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTTCCAGAACTGAGG 1020
Db 961 AGTCTGTGCTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTTCCAGAACTGAGG 1020
Qy 1021 CAGAACAAAGTTGGTGTGAGCTTCCAGCTGGGAGGAGAGATGCCAGGTTGAAAGATCT 1080
Db 1021 CAGAACAAAGTTGGTGTGAGCTTCCAGCTGGGAGGAGAGATGCCAGGTTGAAAGATCT 1080
Qy 1081 GG 1082
Db 1081 GG 1082

RESULT 2

ADB99267

ID ADB99267 standard; cDNA; 1156 BP.

XX ADB99267;

XX 04-DEC-2003 (first entry)

XX Human p2Y21i cDNA.

XX ss; gene; human; P2Y21i; chromosome 3; G protein-coupled receptor; GPCR;
XX Class A rhodopsin-like sub-family; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 21..1106

XX /*tag= a

XX /product= "P2Y21i"

XX DE10144044-A1.

XX 27-MAR-2003.

XX 07-SEP-2001; 2001DE-01044044.

XX 07-SEP-2001; 2001DE-01044044.

XX (BRUE/) BRUESS M.

XX (BOEN/) BOENISCH H.

XX (VKUE/) VON KUEGELGEN I.

XX Bruess M, Boenisch H, Von Kuegelgen I;

XX WPI; 2003-364675/35.

XX P-PSDB; ADB99264.

XX New human gene P2Y21i and encoded G protein-coupled receptor, useful for treatment and diagnosis of receptor-associated diseases and for drug screening.

XX Disclosure; Page 4; 6pp; German.

XX This invention describes the human P2Y21i gene and its 5' - and 3' -
XX untranslated regions, located on chromosome 3 which is a novel G protein-
XX coupled receptor (GPCR). The protein encoded by P2Y21i is expressed in
XX blood cells, testis and embryonal kidney cells and contains potential
XX sites for phosphorylation by protein kinase C and casein kinase II. It is
XX a member of the Class A rhodopsin-like sub-family of G protein-coupled

CC receptors and it probably a nucleoside/nucleotide receptor that mediates
CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2L1 and
CC antibodies directed against the encoded protein are useful in diagnosis
CC and treatment (including gene therapy) of diseases associated with
CC abnormal levels of P2Y2L1 expression, in screening assays for modulators,
CC potential therapeutic agents, and to produce transgenic animals, e.g. for
CC identifying diseases associated with abnormal expression of P2Y2L1. This
CC sequence represents the P2Y2L1 gene described in the disclosure of the
CC invention.

XX
SQ Sequence 1156 BP; 243 A; 335 C; 295 G; 283 T; 0 U; 0 Other;
Query Match 100.0%; Score 1082; DB 10; Length 1156;
Best Local Similarity 100.0%; Pred. No. 4e-285;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTCCATTGTTCTTCCAGGGGAAGCAGAAAGCGGGAGCCGTCTGTGAGCTCTG 60
Db 21 ATGCTGTCCATTGTTCTTCCAGGGGAAGCAGAAAGCGGGAGCCGTCTGTGAGCTCTG 80

Qy 61 CTCTGGAGGAGCCCTCCGGGACATGAGAGGTGAGATGAATACATCAGAGGAACAA 120
Db 81 CTCTGGAGGAGCCCTCCGGGACATGAGAGGTGAGATGAATACATCAGAGGAACAA 140

Qy 121 GGTCCTGCGAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
Db 141 GGTCCTGCGAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 200

Qy 181 ATCTTTATCTAGGCTGCCATTAATGCACTGTCTTGGGCACCTCTGGGGCCAAAC 240
Db 201 ATCTTTATCTAGGCTGCCATTAATGCACTGTCTTGGGCACCTCTGGGGCCAAAC 260

Qy 241 AAGCGTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGTGGCCGACCTGCTTTAT 300
Db 261 AAGCGTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGTGGCCGACCTGCTTTAT 320

Qy 301 GTGCTATGTCCTTCTCATCATCACTACTCATAGATGACAGGTGGCCCTTCGGGGAG 360
Db 321 GTGCTATGTCCTTCTCATCATCACTACTCATAGATGACAGGTGGCCCTTCGGGGAG 380

Qy 361 CTGCTCTGCAAGTGTGTGCACTTCTTCTTATATCAACTTACGCGAGCATCTGTGTG 420
Db 381 CTGCTCTGCAAGTGTGTGCACTTCTTCTTATATCAACTTACGCGAGCATCTGTGTG 440

Qy 421 CTGACCTGCATCTCTGTGCACTGCTCTAGGTGTGTGCACTGCTGCTGCTGCC 480
Db 441 CTGACCTGCATCTCTGTGCACTGCTCTAGGTGTGTGCACTGCTGCTGCTGCC 500

Qy 481 TACGGACCGAGGATGCTGCTGGGCAACGACGACCACTGGCCCTGTGTGCTCTC 540
Db 501 TACGGACCGAGGATGCTGCTGGGCAACGACGACCACTGGCCCTGTGTGCTCTC 560

Qy 541 CAGCTGTGCCCCACACTGGGCTTCTCCACACGAGCTTACATCAATGGCCAGATGATCTG 600
Db 561 CAGCTGTGCCCCACACTGGGCTTCTCCACACGAGCTTACATCAATGGCCAGATGATCTG 620

Qy 601 TATGATGACGAGGCAAGAAATTTGATCGGCTTTTGGCTACGGCATAGTCTTGACA 660
Db 621 TATGATGACGAGGCAAGAAATTTGATCGGCTTTTGGCTACGGCATAGTCTTGACA 680

Qy 661 TTGCTCGCTTCTTCTCCCTGCTGCTATTTGCTGCTATTTACTATGATGTGAGGAG 720
Db 681 TTGCTCGCTTCTTCTCCCTGCTGCTATTTGCTGCTATTTACTATGATGTGAGGAG 740

Qy 721 CCTGATCAAGCCAGAGGAGAACTCTATGAGGACAGGCAACACAGCCGAGCCAGGTCAT 780
Db 741 CCTGATCAAGCCAGAGGAGAACTCTATGAGGACAGGCAACACAGCCGAGCCAGGTCAT 800

Qy 781 CCGGACCATCTACTGTGTGTGCTCTTACCTCTGTTTGTGCTTCCATATCAC 840
Db 801 CCGGACCATCTACTGTGTGTGCTCTTACCTCTGTTTGTGCTTCCATATCAC 860

Qy 841 TCGCTCCTTCTACTCCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGC 900

Db 861 TCGTCTTCTTACTCTACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGC 920
Qy 901 AGCCAGTGTGCGCTTACAGATATAGAGGCTCTCTGTGAGTGTGAGCTCTCAACCC 960
Db 921 AGCCAGTGTGCGCTTACAGATATAGAGGCTCTCTGTGAGTGTGAGCTCTCAACCC 980

Qy 961 AGTCTGTACTTCTTCTTCAAGGGGGCAAAATAGATCAGGCTCTCTCAGAAACTGAGG 1020
Db 981 AGTCTGTACTTCTTCTTCAAGGGGGCAAAATAGATCAGGCTCTCTCAGAAACTGAGG 1040

Qy 1021 CAGAACAGTTGGGTGAGCATCCAGCTGGGAGGAGATGCCAGGGTTGAAACAGATCT 1080
Db 1041 CAGAACAGTTGGGTGAGCATCCAGCTGGGAGGAGAGATGCCAGGGTTGAAACAGATCT 1100

Qy 1081 GG 1082
Db 1101 GG 1102

RESULT 3
ADC86166
ID ADC86166 standard; DNA; 1334 BP.
XX
AC ADC86166;
XX AC
XX 01-JAN-2004 (first entry)
XX
Human GPCR gene SEQ ID NO:619.
XX
ds; gene; human; GPCR;
XX guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX Homo sapiens.
XX
XX EP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX WPI: 2003-315783/31.
XX P-PSDB; ADC86167.
XX
XX New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 619; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The
XX polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
XX invention.
XX
SQ Sequence 1334 BP; 283 A; 368 C; 348 G; 335 T; 0 U; 0 Other;
Query Match 100.0%; Score 1082; DB 10; Length 1334;
Best Local Similarity 100.0%; Pred. No. 4.3e-285;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTCCATTGTTCTTCCAGGGGAAGCAGAAAGCGGGAGCCGTCTGTGAGCTCTG 60

CC modulating the activity of NOVX, treating or preventing a NOVX-associated
 CC disorder, determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX and treating a pathological state
 CC in a mammal comprising administering a polypeptide which is at least 95%
 CC identical to NOVX (or fragment). NOVX and NA may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
 CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
 CC antagonists may also be used to down regulate expression and activity of
 CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
 CC detecting the presence of NOVX in samples (e.g. by enzyme linked
 CC immunosorbent assay (ELISA)). The agents and methods may be used in this
 CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
 CC and/or atherosclerosis. The present sequence encodes a NOVX protein.
 XX
 SQ Sequence 1108 BP; 225 A; 321 C; 285 G; 277 T; 0 U; 0 Other;

Query Match 97.9%; Score 1059; DB 12; Length 1108;
 Best Local Similarity 99.8%; Pred. No. 7.7e-279;
 Matches 1081; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 1 ATGCTGTCATTTTCCTTCCTTCAGGGGAAGCAGAGCGGCGCTCGTGGAGCTCTG 60
 12 ATGCTGTCATTTTCCTTCCTTCAGGGGAAGCAGAGCGGCGCTCGTGGAGCTCTG 71
 61 CTCCTGGAGGAGCCTCCCGGACATGGAGAGGTGGACATGATCATCACAGGAACAA 120
 72 CTCCTGGAGGAGCCTCCCGGACATGGAGAGGTGGACATGATCATCACAGGAACAA 131
 121 GGTCTCTGCCAGTTCTCAGAGAAGTCAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
 132 GGTCTCTGCCAGTTCTCAGAGAAGTCAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 191
 181 ATCTTTATCTAGGCTGCCACTAAATGGCACTGTCTGTGGCACTCCCTGGGCCCAAAAC 240
 192 ATCTTTATCTAGGCTGCCACTAAATGGCACTGTCTGTGGCACTCCCTGGGCCCAAAAC 251
 241 AAGCGCTGGAGCTGTGCCACCACTATCTGTGTGAACCTGTATGTGGCGCACTGCTTTAT 300
 252 AAGCGCTGGAGCTGTGCCACCACTATCTGTGTGAACCTGTATGTGGCGCACTGCTTTAT 311
 301 GTGCTATGGCTTCCTCATCATCATCTACTACTAGATCAGAGTGGCCCTTCGGGGAG 360
 312 GTGCTATGGCTTCCTCATCATCATCTACTACTAGATCAGAGTGGCCCTTCGGGGAG 371
 361 CTGCTCTGCAAGCTGGTGCACTTCTCTTATATCACTTTACGCGACATCTCTGCTG 420
 372 CTGCTCTGCAAGCTGGTGCACTTCTCTTATATCACTTTACGCGACATCTCTGCTG 431
 421 CTGACCTGCACTCTGTGCAACAGTTCCTAGGTGTGTGCAACCACTGTGCTGCTGCC 480
 432 CTGACCTGCACTCTGTGCAACAGTTCCTAGGTGTGTGCAACCACTGTGCTGCTGCC 491
 481 TACCGGACCGCAGCATGTGCTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
 492 TACCGGACCGCAGCATGTGCTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 551
 541 CAGCTGTGCTGCCACACTGGCCTTCTCCACACGAGCTACATCAATGCGCAGATGATCTG 600
 552 CAGCTGTGCTGCCACACTGGCCTTCTCCACACGAGCTACATCAATGCGCAGATGATCTG 611
 601 TATGACATGACCGCAGCAGATTTTGTATGCGCTTTTTCCTACGCGATAGTTCGACA 660
 612 TATGACATGACCGCAGCAGATTTTGTATGCGCTTTTTCCTACGCGATAGTTCGACA 671
 661 TTGCTGCTGCTTCTTCCCTGCTGCTATTTTGGTGTGCTATTTCACTAGTGTCTGAGG 720
 672 TTGCTGCTGCTTCTTCCCTGCTGCTATTTTGGTGTGCTATTTCACTAGTGTCTGAGG 730
 721 CCTGATCAAGCAGCAGAGAACCTCATGAGGACAGGCAACAGCCCGAGCCAGGTCCAT 780
 731 CCTGATCAAGCAGCAGAGAACCTCATGAGGACAGGCAACAGCCCGAGCCAGGTCCAT 790

QY 781 CCGHACCATCTACTGCTGTGTGCTTTCACCTCTGTTTGGCTTCCATATCAC 840
 DB 791 CCGHACCATCTACTGCTGTGTGCTTTCACCTCTGTTTGGCTTCCATATCAC 850
 QY 841 TCGCTCTCTTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGC 900
 DB 851 TCGCTCTCTTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGC 910
 QY 901 AG-CAGGTGTGGCTTACAGATATGAGAGCTCTGTGTGAGTGTGAGAGCTCTCAACC 959
 DB 911 AGCCAGGTGTGGCTTACAGATATGAGAGCTCTGTGTGAGTGTGAGAGCTCTCAACC 970
 QY 960 CAGTCTCTGCTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTCCAGAAACTGAG 1019
 DB 971 CAGTCTCTGCTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTCTCCAGAAACTGAG 1030
 QY 1020 GCAGAACAGTTGGTGTGAGTCCAGCTGGGAGAGAGATGCCAGGTTTGAACAGATC 1079
 DB 1031 GCAGAACAGTTGGTGTGAGTCCAGCTGGGAGAGAGATGCCAGGTTTGAACAGATC 1090
 QY 1080 TGG 1082
 DB 1091 TGG 1093
 RESULT 7
 AAS98135
 ID AAS98135 standard; DNA; 1063 BP.
 XX AAS98135;
 XX AC
 XX DT 12-MAR-2002 (first entry)
 XX DE Human DNA for potential G protein-coupled receptor #92.
 XX KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
 KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
 KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
 KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
 KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
 KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
 KW tuberculosis; cognition disorder; memory disorder; anorexia;
 KW hormonal release disorder; cardiovascular activity disorder;
 KW pain perception disorder; obesity; diabetes; diabetes; obesity; diabetes;
 KW hyperlipidaemia; stroke; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200185791-A1.
 XX PD 15-NOV-2001.
 XX PF 11-MAY-2001; 2001WO-US015332.
 XX PR 11-MAY-2000; 2000US-0203217P.
 PR 18-MAY-2000; 2000US-0205945P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX PI Brown JP, Miller M, Burmer G, Fabre-Suver C, Pritchard D;
 XX WPI; 2002-065595/09.
 XX PT Novel G protein-coupled receptor polypeptides including galanin receptor
 PT polypeptides useful for identifying modulators that are useful for
 PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
 PT stroke.
 XX PS Claim 2; Page 98; 144pp; English.
 XX CC The invention relates to an isolated polypeptide encoded by a nucleic
 CC acid molecule that is at least 80% identical to the G protein-coupled

CC (GPCR) polynucleotides included in the specification. Also included are
 CC probes based on the GPCR sequences (including antisense probes), a host
 CC cell comprising an expression vector comprising the GPCR sequence,
 CC antibodies raised against the polypeptides, and methods of identifying
 CC modulators of the polypeptides. The polypeptides are useful for
 CC identifying modulator compounds which function as modulators, activators,
 CC repressors, agonists or antagonists of the novel GPCR polypeptides
 CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as
 CC described above can be used to detect the presence of the polypeptides
 CC and nucleic acids and are used to diagnose a variety of diseases or
 CC disorders in which GPCRs are involved e.g., Alzheimer's disease,
 CC anyotropic lateral sclerosis, asthma, atherosclerosis, basal cell
 CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
 CC obstructive pulmonary disease, Crohn's disease, depression, epilepsy,
 CC macular degeneration, lymphoma, melanoma, multiple sclerosis,
 CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, and many other
 CC diseases listed in the specification. The probes and antibodies are also
 CC useful for diagnosing cognition and memory disorders, anorexia, hormonal
 CC release disorders, cardiovascular activity disorders, pain perception
 CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
 CC that decrease or increase the expression of galanin receptor (GAL4) can
 CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
 CC nucleic acid is useful for treating the above mentioned disorders by gene
 CC therapy techniques. The present sequence is a novel GPCR polynucleotide
 CC of the invention
 XX
 SQ Sequence 1063 BP; 216 A; 315 C; 272 G; 260 T; 0 U; 0 Other;
 Query Match 97.1%; Score 1051; DB 6; Length 1063;
 Best Local Similarity 99.9%; Pred. No. 1.2e-276;
 Matches 1062; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 19 CCTTCAGGGGAGCAGAGCGGAGCGCTGCTGGAGCTCTGCTCTGGAGGAGCGCTCC 78
 DB 1 CCTTCAGGGGAGCAGAGCGGAGCGCTGCTGGAGCTCTGCTCTGGAGGAGCGCTCC 60
 QY 79 CGGACATGAGAGGTGGACATGATATACATACAGGACAAAGCTCTCTGCCAGTTCTCA 138
 DB 61 CGGACATGAGAGGTGGACATGATATACATACAGGACAAAGCTCTCTGCCAGTTCTCA 120
 QY 139 GAGAAGTACAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTG 198
 DB 121 GAGAAGTACAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTG 180
 QY 199 CCACTAATGGCACTCTCTGTCGCACTCTGGGCGCAACCAAGCGCTGGAGCTGTGC 258
 DB 181 CCACTAATGGCACTCTCTGTCGCACTCTGGGCGCAACCAAGCGCTGGAGCTGTGC 240
 QY 259 ACCACCTATCTGTGAACTGTGTCGCACTCTGTTTATGTCTATTGCTTCCCTCCCTC 318
 DB 241 ACCACCTATCTGTGAACTGTGTCGCACTCTGTTTATGTCTATTGCTTCCCTCCCTC 300
 QY 319 ATCATCACTACTACTAGATGACGTGGCCCTTCTGGGAGCTGCTTGCAGCTGGTG 378
 DB 301 ATCATCACTACTACTAGATGACGTGGCCCTTCTGGGAGCTGCTTGCAGCTGGTG 360
 QY 379 CACTTCTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCTCTCTG 438
 DB 361 CACTTCTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCTCTCTG 420
 QY 439 CACAGTTCCTAGTGTGTGCCACCACTGTTGTCGCTCCCTACCGACCCCGACGAT 498
 DB 421 CACAGTTCCTAGTGTGTGCCACCACTGTTGTCGCTCCCTACCGACCCCGACGAT 480
 QY 499 GCGTGGTGGGACCAACCACTGCGCCCTGGTGTCTCCAGTGTGCTGCCACACTG 558
 DB 481 GCGTGGTGGGACCAACCACTGCGCCCTGGTGTCTCCAGTGTGCTGCCACACTG 540
 QY 559 GCGTTCCTCCACAGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAC 618
 DB 541 GCGTTCCTCCACAGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAC 600

QY 619 GAGAATTTTGATCGGCTTTTTCCTACGGCATAGTTCTGACATGTCTGGCTTCTTTTCC 678
 DB 601 GAGAATTTTGATCGGCTTTTTCCTACGGCATAGTTCTGACATGTCTGGCTTCTTTTCC 660
 QY 679 CTCCTTGGTCAATTTTGGTGTGCTATTCACTGATGCTGAGGCTGATCAAGCCAGAGGA 738
 DB 661 CTCCTTGGTCAATTTTGGTGTGCTATTCACTGATGCTGAGGCTGATCAAGCCAGAGGA 720
 QY 739 GAACCTCATGAGGACAGCAACACAGCCCGAGCGAGTCCATCCGACCATCTACTGGT 798
 DB 721 GAACCTCATGAGGACAGCAACACAGCCCGAGCGAGTCCATCCGACCATCTACTGGT 780
 QY 799 GTGTGGCTCTTCAACCTCTGTTTGTGCTTCCATATCATCTGCTCTTACCTCAC 858
 DB 781 GTGTGGCTCTTCAACCTCTGTTTGTGCTTCCATATCATCTGCTCTTACCTCAC 840
 QY 859 CATCTGCTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAG-CCAGTGTGGCCTTACA 917
 DB 841 CATCTGCTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCCTTACA 900
 QY 918 AGATATGAGGAGCTCTGGTGTGAGTGTGAGCAGCTCCCTCAACCCAGTCTGTACTTCTTT 977
 DB 901 AGATATGAGGAGCTCTGGTGTGAGTGTGAGCAGCTCCCTCAACCCAGTCTGTACTTCTTT 960
 QY 978 CAAGGGGGGCAAAAATAGAGTCAAGCTCCTCCAGAACTGAGGCGAGAACTGGGTGGA 1037
 DB 961 CAAGGGGGGCAAAAATAGAGTCAAGCTCCTCCAGAACTGAGGCGAGAACTGGGTGGA 1020
 QY 1038 GCATCCAGCTGGGAGGAGAGATGCCAGGGTTGAAAGATCT 1080
 DB 1021 GCATCCAGCTGGGAGGAGAGATGCCAGGGTTGAAAGATCT 1063

RESULT 8
 ADC25999 standard; DNA; 1017 BP.
 XX
 AC ADC25999;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human purinergic receptor P2Y-related GPCR \times 6 DNA.
 KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
 KW anorectic; cardiant; hypotensive; osteopathic; antiangiogenic;
 KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
 KW neurotropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
 KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
 KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
 KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
 KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
 KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
 KW human; GPCR \times 6; purinergic receptor P2Y; ds; gene.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..1017
 /tag= a
 /product= "Human purinergic receptor P2Y-related GPCR \times 6
 protein - both "original" and "alternative" versions"
 /transl_except= (pos:184..186, aa:Pro)
 /transl_except= (pos:727..729, aa:Xaa)
 /transl_except= (pos:808..810, aa:Pro)
 /note= "Xaa = Unknown; translation exceptions at 184 and
 727 are present within "original" protein CDS whilst that
 at 808 is present within the "alternative" protein CDS"
 XX
 FN US2003088080-A1.
 XX
 PD 08-MAY-2003.
 XX
 XX 21-JUN-2001; 2001US-00885453.
 PF

Db	481	TACCGGACCGGAGCATGCTGGCTGGGCAACGACCACTTGGCCCTTGTTGGTCCCTC	540
Qy	541	CAGCTGTGCGCCACATGGCCCTTCCCAACAGGACTACATCAATGGCCAGATGATCTGG	600
Db	541	CAGCTGCTGCGCCACATGGCCCTTCCCAACAGGACTACATCAATGGCCAGATGATCTGG	600
Qy	601	TATGACATGACCGCCAGAGAAATTTGATCGGCTTTTTCGCTACGGCATAGTCTTGACA	660
Db	601	TATGACATGACCGCCAGAGAAATTTGATCGGCTTTTTCGCTACGGCATAGTCTTGACA	660
Qy	661	TTGTCTGGCTTTCTTTCCCTCCCTTGGTCAATTTTGGTGTGCTATTCACTGATGCTCAGGAG	720
Db	661	TTGTCTGGCTTT- TTTCCCTCCTTGGTCAATTTTGGTGTGCTATTCACTGATGCTCAGGAG	719
Qy	721	CTGTATCAGCCAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCAT	780
Db	720	CTGTATCAGCCAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCAT	779
Qy	781	CCGGACCACTCTACTTGGTGTGGCCCTTTCACCCCTGTGTTTGTGCCCTTCCATATCAC	840
Db	780	CCGGACCACTCTACTTGGTGTGGCCCTTTCACCCCTGTGTTTGTGCCCTTCCATATCAC	839
Qy	841	TGCTCTCTTCTACTCACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGC	900
Db	840	TGCTCTCTTCTACTCACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGC	899
Qy	901	ASCCAGTGTGGCTACAGATATGAGAGCCCTCTGGTGTGAGTGTCAGAGCTGCGCTCAACCC	960
Db	900	ASCCAGTGTGGCTACAGATATGAGAGCCCTCTGGTGTGAGTGTCAGAGCTGCGCTCAACCC	959
Qy	961	AGTCTCTGACTTTCTTTCAAGGGGGCAAAATAGAGTCTAGGCTCTCCAGAAACTGA	1018
Db	960	AGTCTCTGACTTTCTTTCAAGGGGGCAAAATAGAGTCTAGGCTCTCCAGAAACTGA	1017
RESULT 9			
AAD61648			
ID AAD61648 standard; DNA; 1017 BP.			
XX	AAD61648;		
XX	AC AC		
XX	15-JAN-2004 (first entry)		
DT	Human GPCR6 DNA.		
XX	Human; G-protein coupled receptor; GPCR; infection; neoplastic process;		
KW	inflammation; myocardial infarction; atherosclerosis; angina pectoris;		
KW	hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;		
KW	diabetes; cancer; virucide; analgesic; cardiant; gene; ds.		
XX	Homo sapiens.		
OS	Key		
XX	Location/Qualifiers		
FT	1..1017		
FT	/*tag= a		
FT	/product= "Human GPCR protein"		
XX	US2003108986-A1.		
PN	12-JUN-2003.		
XX	20-FEB-2002; 2002US-00079384.		
XX	21-JUN-2001; 2001US-00885453.		
XX	(EURO-) EUROSREEN SA.		
PA	Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;		
PI	Govaerts C;		
PI	WPI; 2003-810852/76.		
XX	P-PSDB; ABW00804.		
DR			

Query Match		92.7%; Score 1002.8; DB 6; Length 1020;
Best Local Similarity		99.6%; Pred. No. 1.7e-263;
Matches 1016; Conservative 0; Mismatches 2; Indels 2; Gaps 1;		
Qy	1	ATGCTGTCCATTTTCTCTTCCCTCAGGGGAGCAGAGAGCGGAGCCCTGCTGAGCTCTG 60
Db	1	ATGCTGTCCATTTTCTCTTCCCTCAGGGGAGCAGAGAGCGGAGCCCTGCTGAGCTCTG 60
Qy	61	CTCTGAGGAGGCTCCCGGACATGAGAGAGTGGACATGATATACATACAGGACAA 120
Db	61	CTCTGAGGAGGCTCCCGGACATGAGAGAGTGGACATGATATACATACAGGACAA 120
Qy	121	GGTCTCTGCCAGTCTCAGAGAGTACAGCAAGTCTACCTCTCTCCCTGGCTACAGTATC 180
Db	121	GGTCTCTGCCAGTCTCAGAGAGTACAGCAAGTCTACCTCTCTCCCTGGCTACAGTATC 180
Qy	181	ATCTTTATCTAGGCTGCCACTAAATGGCACTCTCTTTGTGGCACTCTCTGGGGCCAAAC 240
Db	181	ATCTTTATCTAGGCTGCCACTAAATGGCACTCTCTTTGTGGCACTCTCTGGGGCCAAAC 240
Qy	241	AAGCGCTGGAGCTGTGCCACCACTATCTGTGGAACCTGATGTGGCGGACCTGCTTTAT 300
Db	241	AAGCGCTGGAGCTGTGCCACCACTATCTGTGGAACCTGATGTGGCGGACCTGCTTTAT 300
Qy	301	GTGCTATTGCCCTTCTCATCATCACCTACTCTAGTAGACAGGTTGGCCCTTCGGGGAG 360
Db	301	GTGCTATTGCCCTTCTCATCATCACCTACTCTAGTAGACAGGTTGGCCCTTCGGGGAG 360
Qy	361	CTGCTCTGACAGCTGTGCACTCTCTCTATATCAACCTTTACGCGACATCTCTGCTG 420
Db	361	CTGCTCTGACAGCTGTGCACTCTCTCTATATCAACCTTTACGCGACATCTCTGCTG 420
Qy	421	CTGACCTGCTCTCTGTCACCACTCTCTAGTGTGTGCCACCACTCTGTTTCGCTGCC 480
Db	421	CTGACCTGCTCTCTGTCACCACTCTCTAGTGTGTGCCACCACTCTGTTTCGCTGCC 480
Qy	481	TACCGGACCGCAGGATGCTGCTGGGACACGACCACTGTTGGCCCTTGTGTTCTC 540
Db	481	TACCGGACCGCAGGATGCTGCTGGGACACGACCACTGTTGGCCCTTGTGTTCTC 540
Qy	541	CAGCTGTGCTCCACACTGGGCTTCTCCACACGAGTACATCAATGCGCAGATGATCTGG 600
Db	541	CAGCTGTGCTCCACACTGGGCTTCTCCACACGAGTACATCAATGCGCAGATGATCTGG 600
Qy	601	TATGACATGACAGCCAGAGAAATTTTGTGCTGCTTTTTCCTACGCACTGATCTGACA 660
Db	601	TATGACATGACAGCCAGAGAAATTTTGTGCTGCTTTTTCCTACGCACTGATCTGACA 660
Qy	661	TTGCTGCTCTCTCTT--CCCTCTGCTGCTATTTTGGTGTGCTATTCACCTGATGTCAGG 718
Db	661	TTGCTGCTCTCTCTT--CCCTCTGCTGCTATTTTGGTGTGCTATTCACCTGATGTCAGG 720
Qy	719	AGCTGTATCAAGCCAGAGGAACTCATGAGGACAGGACAGCCGAGCCAGGCTCC 778
Db	721	AGCTGTATCAAGCCAGAGGAACTCATGAGGACAGGACAGCCGAGCCAGGCTCC 780
Qy	779	ATCCGGACCATCTACTGTTGTGGCTCTTCAACCTCTGTTTGTGCTCCATATC 838
Db	781	ATCCGGACCATCTACTGTTGTGGCTCTTCAACCTCTGTTTGTGCTCCATATC 840
Qy	839	ACTGCTCTCTTACCTCACCATCTGCTCTCTGCTTTCTCAGGACTGCCAGCTCTGATG 898
Db	841	ACTGCTCTCTTACCTCACCATCTGCTCTCTGCTTTCTCAGGACTGCCAGCTCTGATG 900
Qy	899	GCAGCAGTGTGGCTACAGATATGAGGCTCTCTGTTGATGTGACAGCTGCTCTCAAC 958
Db	901	GCAGCAGTGTGGCTACAGATATGAGGCTCTCTGTTGATGTGACAGCTGCTCTCAAC 960
Qy	959	CCAGTCTGTACTTCTTCTCAAGGGGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1018
Db	961	CCAGTCTGTACTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1020

RESULT 11	
AAD29667	
ID	AAD29667 standard; cDNA; 1076 BP.
XX	AC AAD29667;
XX	DT 17-MAY-2002 (first entry)
XX	DE Human G-protein coupled receptor (GCRC-1) cDNA.
XX	Human; G-protein coupled receptor; GCRC-1; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease; Pick's disease; Huntington's disease; Parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crhn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant; neurotropic; neuroprotective; cardiac; immunosuppressive; anorectic; viricide; gene; ss.
XX	OS Homo sapiens.
XX	Key Location/Qualifiers
FT	CDS 57..1076
FT	/*tag= a
FT	/product= "Human GCRC-1"
XX	WO200210387-A2.
XX	07-FEB-2002.
XX	25-JUL-2001; 2001WO-US023433.
XX	27-JUL-2000; 2000US-0221478P.
XX	03-AUG-2000; 2000US-023268P.
XX	21-AUG-2000; 2000US-0227054P.
XX	08-SEP-2000; 2000US-0231121P.
XX	13-SEP-2000; 2000US-023243P.
XX	15-SEP-2000; 2000US-0232691P.
XX	22-SEP-2000; 2000US-0235146P.
XX	(INCY-) INCYTE GENOMICS INC.
XX	Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
XX	Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;
XX	Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC;
XX	Warren BA, Lee EA, Ding L;
XX	WPI: 2002-188744/24.
XX	P-PSDB; AAE18640.
XX	New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders.
XX	Claim 5; Page 137-138; 150pp; English.
XX	The invention relates to novel human G-protein coupled receptors (GCRC) and their encoding polynucleotides. GCRC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCRC is useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., hepatitis, psoriasis, cancer); a neurological disorder (e.g., epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crhn's disease), an autoimmune/inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infections. GCRC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell

CC type. GCREC is useful for creating knockin humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene
CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion, etc., among normal, carrier or affected individuals, and as
CC hybridization probes for mapping naturally occurring genomic sequences.
CC GCREC is useful in Southern or northern analysis, dot blot or other
CC membrane-based technologies, in PCR technologies, in dipstick, pin,
CC microformat enzyme linked immunosorbant (ELISA)-like assays, and in
CC microarrays utilising fluids or tissues from patients to detect altered
CC GCREC expression. The present sequence is human GCREC-1 cDNA
XX
SQ Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;

Query Match 92.7%; Score 1002.8; DB 6; Length 1076;
Best Local Similarity 99.6%; Pred. No. 1-7e-263;
Matches 1016; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 1 ATGCTGCCATTTTGTCTCTTCCAGGGGAAGCAGAGCGGAGCGTCTGTGAGCTCTG 60
Db 57 ATGCTGCCATTTTGTCTCTTCCAGGGGAAGCAGAGCGGAGCGTCTGTGAGCTCTG 116
Qy 61 CTCTGGAGGAGCCCTCCGGGACATGGAGAGGTGGACATGATACATCACAGGAACAA 120
Db 117 CTCTGGAGGAGCCCTCCGGGACATGGAGAGGTGGACATGATACATCACAGGAACAA 176
Qy 121 GGTCTCTGCCAGTTCTCAGAGAAGTACAAGCAAGTCTTACCTCTCCCTGGCCTACAGTATC 180
Db 177 GGTCTCTGCCAGTTCTCAGAGAAGTACAAGCAAGTCTTACCTCTCCCTGGCCTACAGTATC 236
Qy 181 ATCTTTATCTAGGCTGACCAATGAGCACTGTCTTGGGACACTCTCTGGGCGCAAAAC 240
Db 237 ATCTTTATCTAGGCTGACCAATGAGCACTGTCTTGGGACACTCTCTGGGCGCAAAAC 296
Qy 241 AAGCGGTGAGCTGTGGACCACTATCTGGTGAACCTGATGTGGCGACCTGCTTTAT 300
Db 297 AAGCGGTGAGCTGTGGACCACTATCTGGTGAACCTGATGTGGCGACCTGCTTTAT 356
Qy 301 GTGCTATTGCGCTTCATCATCATCATCTATCTAGTAGACAGGTGGCCCTTCGGGGAG 360
Db 357 GTGCTATTGCGCTTCATCATCATCATCTATCTAGTAGACAGGTGGCCCTTCGGGGAG 416
Qy 361 CTGCTCTGCAAGCTGTGGCACTCTCTCTATATCAACCTTTACGGCAGCATCTGCTG 420
Db 417 CTGCTCTGCAAGCTGTGGCACTCTCTCTATATCAACCTTTACGGCAGCATCTGCTG 476
Qy 421 CTGACCTGCATCTCTGTGCCAGTCTCTAGGTGTGTGCCACCACTGTGCTGCTGCC 480
Db 477 CTGACCTGCATCTCTGTGCCAGTCTCTAGGTGTGTGGCAGCAGCATCTGCTGCC 536
Qy 481 TACGGACCCGAGGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
Db 537 TACGGACCCGAGGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 596
Qy 541 CAGCTGTGCCACACTGGCTCTCTCCACACGAGCTACATCAATGGCCAGATGATCTGG 600
Db 597 CAGCTGTGCCACACTGGCTCTCTCCACACGAGCTACATCAATGGCCAGATGATCTGG 656
Qy 601 TATGACATGACACGCAAGAGAAATTTGATGCTGCTTTTGGCTACGCGCATAGTCTGACA 660
Db 657 TATGACATGACACGCAAGAGAAATTTGATGCTGCTTTTGGCTACGCGCATAGTCTGACA 716
Qy 661 TTGCTGCTCTCTCTT--CCCTCTCTGCTATTTTGGTGTGCTATTCACTGATGCTCAGG 718
Db 717 TTGCTGCTCTCTCTTCCCTCTCTTGGTGTGCTATTCACTGATGCTCAGG 776
Qy 719 AGCTGTATCAAGCAGGAGAGAACTCATGAGGACAGGCAACACAGCCGAGCAGGTCC 778
Db 777 AGCTGTATCAAGCAGGAGAGAACTCATGAGGACAGGCAACACAGCCGAGCAGGTCC 836
Qy 779 ATCCGACCATCTCTGCTGTGGCTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 838
Db 837 ATCCGACCATCTCTGCTGTGGCTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 896

Qy 839 ACTGCTCTCTTCTACCTACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATG 898
Db 897 ACTGCTCTCTTCTACCTACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATG 956
Qy 899 GGAGCAGTGTGGCTTCAAGATATGAGAGGCTCTGTTGAGTGTGAGCAGTGTGCTCAAC 958
Db 957 GCACCCAGTGTGGCTTCAAGATATGAGAGGCTCTGTTGAGTGTGAGCAGTGTGCTCAAC 1016
Qy 959 CCAGTCCGTGATCTTCTTCAAGGGGGGCAAAATAGAGTCTGCTCCAGAACTGA 1018
Db 1017 CCAGTCCGTGATCTTCTTCAAGGGGGGCAAAATAGAGTCTGCTCCAGAACTGA 1076

RESULT 12

ADO30395 standard; cDNA; 1076 BP.

XX ADO30395;

XX 29-JUL-2004 (first entry)

XX Human GPCR P2Y3L polynucleotide, SEQ ID NO:1498.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
XX cystostatic; antiinflammatory; vasotropic; antidiarrhoeic; antiarrhythmic;
XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
XX virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
XX dermatological; antitumor; antithyroid; antiallergic; anorectic;
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
XX Gene; ss.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX P-PSDB; ADO30394.

XX Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition

PT associated with GPCR dysfunction e.g. autoimmune diseases, angina

PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1498; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors

CC (GPCRs) and nucleic acids encoding them. The invention also relates to

CC sequences at least 90% identical to the GPCR proteins and nucleic acids

CC of the invention; methods of treating, preventing or diagnosing diseases

CC associated with GPCRs of the invention; methods of screening for

CC compounds useful in the treatment of GPCR-related diseases; a transgenic

CC mouse comprising a GPCR gene of the invention; a mouse comprising a

657	TATGACATGACCGACGAGAAATTTTGATCGGCTTTTGGCTTACGCGCATAGTCTTGACA	716
Qy	TTGTCTGGCTTTCTTTT - CCCTCCTTGGTCATTTTGGTGTGCTATTCACTGATGGTCAGG	718
Db	TTGTCTGGCTTTCTTTTCCCTCCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAGG	776
Qy	AGCCTGATCAAGCCAGAGAGAACCTCATGAGACAGGCAACACAGCCGCGAGCCAGGTCC	778
Db	AGCCTGATCAAGCCAGAGAGAACCTCATGAGACAGGCAACACAGCCGCGAGCCAGGTCC	836
Qy	ATCCGACCAATCTACTGTGTGTGGCTTTCACCTCTGTTTTGTGGCTTCCCATATC	838
Db	ATCCGACCAATCTACTGTGTGTGGCTTTCACCTCTGTTTTGTGGCTTCCCATATC	896
Qy	ACTCGCTCTTCTACCTCACCATCTGCTTTCTCAGGACCTGCCAGCTCTTTGATG	898
Db	ACTCGCTCTTCTACCTCACCATCTGCTTTCTCAGGACCTGCCAGCTCTTTGATG	956
Qy	GCAGCCAGTGTGGCTTCAAGATATGGAGGCTCTGGTGAAGTGTGACGAGCTGCCTCAAC	958
Db	GCAGCCAGTGTGGCTTCAAGATATGGAGGCTCTGGTGAAGTGTGACGAGCTGCCTCAAC	1016
Qy	CCAGTCTCTACTTTTCTTTTCAAGGGGGGAAAAATAGCTCAGGCTTCTCCAGAAACTGA	1018
Db	CCAGTCTCTACTTTTCTTTTCAAGGGGGGAAAAATAGCTCAGGCTTCTCCAGAAACTGA	1076

RESULT 13	
AAH73516	
ID	AAH73516 standard; DNA; 1002 BP.
XX	
XX	AAH73516;
XX	
AC	
AC	
XX	
XX	25-SEP-2001 (first entry)
DT	
DT	
XX	
DE	Human G protein-coupled receptor GPRv71 coding sequence.
XX	
XX	Human; guanosine triphosphate binding protein-coupled receptor;
KW	G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;
KW	GPRv47; GPRv51; GPRv71; GPRv72; cancer; liver cirrhosis;
KW	Alzheimer's disease; cytostatic; hepatotropic; neurotropic;
KW	neuroprotective; gene therapy; peptide therapy; ds.
XX	
XX	
CS	Homo sapiens.
XX	
XX	WO200148188-A1.
PN	
XX	
PD	05-JUL-2001.
XX	
XX	28-DEC-2000; 2000WO-JP009408.
PF	
XX	
XX	28-DEC-1999; 99JP-00375152.
PR	
PR	31-MAR-2000; 2000JP-00101339.
XX	
XX	(HELI-) HELIX RES INST.
PA	
XX	
XX	Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
PI	
XX	
XX	WPI; 2001-425662/45.
DR	P-PSDB; AAG64125.
DR	
XX	
PT	New DNA encoding guanosine triphosphate binding protein coupled receptors
PT	and their expression products for screening potential anticancer and
PT	neurotropic drugs and in diagnosis of these diseases.
XX	
XX	Example 1; Page 142-143; 170pp; Japanese.
PS	
XX	
CC	The invention relates to nine human guanosine triphosphate binding
CC	protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC	GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes
CC	encoding them. These genes and proteins and antibodies against the
CC	protein are useful in the treatment, prevention, diagnosis and

CC	investigation of diseases associated with G protein-coupled receptors, including cancer, cirrhosis of the liver and Alzheimer's disease. The present sequence is a G protein-coupled receptor coding sequence of the invention									
XX										
SQ	Sequence 1002 Bp; 207 A; 293 C; 249 G; 253 T; 0 U; 0 Other;									
	Query Match	92.1%;	Score	996.4;	DB	4;	Length	1002;		
	Best Local Similarity	99.9%;	Pred. No.	9.5e-262;						
	Matches	997;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	85	ATGGAGAAGTGGACATGATATACATACAGGAAACAAAGTCTCTGCCAGTTCACAGAAAG	144							
DB	1	ATGGAGAAGTGGACATGATATACATACAGGAAACAAAGTCTCTGCCAGTTCACAGAAAG	60							
QY	145	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATATCTTTATCTAGGGCTGCCACTA	204							
DB	61	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATATCTTTATCTAGGGCTGCCACTA	120							
QY	205	AATGGCACTCTCTGTGGCACTCTCTGGGCAACCAAGCGTGGAGCTGTGCCACACC	264							
DB	121	AATGGCACTCTCTGTGGCACTCTCTGGGCAACCAAGCGTGGAGCTGTGCCACACC	180							
QY	265	TATCTGGTGAACCTGATGTGGCGACCTGCTTTATGTGCTATGTGCCCTTCTCATCATC	324							
DB	181	TATCTGGTGAACCTGATGTGGCGACCTGCTTTATGTGCTATGTGCCCTTCTCATCATC	240							
QY	325	ACCTACTCTACATGACAGGTGGCCCTTGGGGAGCTGCTGCAAGCTGTGCACTTC	384							
DB	241	ACCTACTCTACATGACAGGTGGCCCTTGGGGAGCTGCTGCAAGCTGTGCACTTC	300							
QY	385	CTGTCTTATATCAACCTTTACGGCAGCATCTCTGCTGACCTGCTATCTGTGCAACAG	444							
DB	301	CTGTCTTATATCAACCTTTACGGCAGCATCTCTGCTGACCTGCTATCTGTGCAACAG	360							
QY	445	TTCTTAGTGTGTGCCACCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	504							
DB	361	TTCTTAGTGTGTGCCACCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420							
QY	505	CTGGGACACGACCACTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	564							
DB	421	CTGGGACACGACCACTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480							
QY	565	TCCACACGCACTATCAATAGCCAGATGATCTGGTATGACATGACATGCCAGCCAGAAAT	624							
DB	481	TCCACACGCACTATCAATAGCCAGATGATCTGGTATGACATGACATGCCAGCCAGAAAT	540							
QY	625	TTTGATCGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTG	684							
DB	541	TTTGATCGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTG	600							
QY	685	GGTCATTTTGGTGTCTATTCTACTGATGGTTCAGGAGCTGATCAAGCCAGAGGAAACCT	744							
DB	601	GGTCATTTTGGTGTCTATTCTACTGATGGTTCAGGAGCTGATCAAGCCAGAGGAAACCT	660							
QY	745	CATGAGACAGGCAACACAGCCGAGCGAGTGCATCCGACCATCTACTGTGTGTGG	804							
DB	661	CATGAGACAGGCAACACAGCCGAGCGAGTGCATCCGACCATCTACTGTGTGTGG	720							
QY	805	CCTCTTCACCTCTGTTTGTGGCTTCCATATACATGCTGCTCTCTACTCCACCATCTG	864							
DB	721	CCTCTTCACCTCTGTTTGTGGCTTCCATATACATGCTGCTCTCTACTCCACCATCTG	780							
QY	865	CTTCTCTGCTTCTCAGACCTGCGAGCTCTCTGATGGCAGCCAGTGTGGCTTACAGATATG	924							
DB	781	CTTCTCTGCTTCTCAGACCTGCGAGCTCTCTGATGGCAGCCAGTGTGGCTTACAGATATG	840							
QY	925	GAGCCCTCTGGTGTGAGTGTGAGCTGCTCTCAACCCAGTCTCTACTCTTTTCAAGGGG	984							
DB	841	GAGCCCTCTGGTGTGAGTGTGAGCTGCTCTCAACCCAGTCTCTACTCTTTTCAAGGGG	900							
QY	985	GGCAAAAATAGTTCAGGCTCTCTCCAGAAATCTGAGGCGAGAAAGTTGGTGTGACATCCA	1044							

Db	901	GGCAAAAATAGAGTTCAGGCTCTCTCCAGAAATCTGAGGCGAGAAAGTTGGTGTGACATCCA	960
Qy	1045	GCTGGGAGGAGACAGATGCCAGGTTGAAACAGATCTGG	1082
Db	961	GCTGGGAGGAGACAGATGCCAGGTTGAAACAGATCTGG	998
RESULT 14			
AAS17747			
ID	AAS17747 standard; DNA; 850 BP.		
XX	AC	AAS17747;	
XX	DT	26-FEB-2002 (first entry)	
XX	DE	Human P2Y-like G protein-coupled receptor exon 1.	
XX	XX	Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD; chronic obstructive pulmonary disease; nervous system disease; Parkinson's disease; multiple sclerosis; dementia; stroke; Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence; bacterial infection; fungal infection; protozoan infection; viral infection; pain; cancer; anorexia; bulimia; asthma; exon 1; acute heart failure; hypotension; hypertension; osteoporosis; diabetes; angina pectoris; myocardial infarction; ulcer; inflammation; allergy; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; delirium; severe mental retardation; dyskinesia.	
XX	OS	Homo sapiens.	
XX	FN	WO200185764-A2.	
XX	PD	15-NOV-2001.	
XX	XX	09-MAY-2001; 2001WO-EP005244.	
XX	PR	11-MAY-2000; 2000US-0203582P.	
XX	PR	21-FEB-2001; 2001US-0269857P.	
XX	XX	(FARB) BAYER AG.	
XX	PI	Ramakrishnan S;	
XX	XX	WPI; 2002-075242/10.	
XX	PT	New polynucleotides for producing P2Y-like G protein-coupled receptors (GPCR) that are used for screening inhibitors or regulators of human P2Y-like GPCR, especially useful for treating pain, cancer or neurological disorders.	
XX	PS	Claim 1; Fig 4; 114pp; English.	
XX	CC	The invention relates to an isolated polynucleotide encoding a P2Y-like G protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or allele, a host cell containing an expression vector comprising the polynucleotide and screening for agents that regulate the GPCR activity. The polynucleotide is useful for producing P2Y-like GPCR polypeptide, which may be employed for screening agents that inhibit or regulate human P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is useful for treating or ameliorating P2Y-like GPCR disorders, particularly COPD (chronic obstructive pulmonary disease), peripheral or central nervous system disease (e.g. Parkinson's disease, multiple sclerosis, dementia, stroke, Alzheimer's disease and many other diseases and disorders listed in the specification), benign prostatic hyperplasia or urinary incontinence. A pharmaceutical composition containing the modulators and/or regulators of P2Y-like GPCR is useful for modulating the activity of a P2Y-like GPCR. In particular, these are useful for treating, preventing or ameliorating infections (e.g. bacterial, fungal, protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma, acute heart failure, hypotension, hypertension, osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcers, inflammation, allergies, psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic depression, delirium, severe mental retardation or dyskinesias). The	

CC present sequence is exon 1 of the P2Y-like GPCR of the invention
 SQ Sequence 850 BP; 165 A; 262 C; 201 G; 222 T; 0 U; 0 Other;
 Query Match 78.6%; Score 850; DB 6; Length 850;
 Best Local Similarity 100.0%; Pred. No. 9.2e-222;
 Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 85 ATGAGAGAGTGGACATGATACATACAGAGAGAGTCTGCGCAGTTCTCAGAGAG 144
 Db 1 ATGAGAGAGTGGACATGATACATACAGAGAGAGTCTGCGCAGTTCTCAGAGAG 60
 QY 145 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGATCATCTTTATCTTAGGGCTGCCACTA 204
 Db 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGATCATCTTTATCTTAGGGCTGCCACTA 120
 QY 205 AATGGCACTGCTTTGTGGCACTCTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCA 264
 Db 121 AATGGCACTGCTTTGTGGCACTCTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCA 180
 QY 265 TATCTGTGACCTGATGGTGGCGACCTGCTTTATCTTAGGGCTGCCACTA 324
 Db 181 TATCTGTGACCTGATGGTGGCGACCTGCTTTATCTTAGGGCTGCCACTA 240
 QY 325 ACCTACTACTAGATGACAGTGGCCCTCTGGGGAGCTGCTCTGCAAGCTGTGCACTTC 384
 Db 241 ACCTACTACTAGATGACAGTGGCCCTCTGGGGAGCTGCTCTGCAAGCTGTGCACTTC 300
 QY 385 CTGTTCTATATCACTTTACGGAGAGATCTGCTGCTGCAAGCTGTGCACTTC 444
 Db 301 CTGTTCTATATCACTTTACGGAGAGATCTGCTGCTGCAAGCTGTGCACTTC 360
 QY 445 TTCCTAGTGTGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
 Db 361 TTCCTAGTGTGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 505 CTGGGACACAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
 Db 421 CTGGGACACAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 565 TCCACACGAGTACATCAATGGCCAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
 Db 481 TCCACACGAGTACATCAATGGCCAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 625 TTTGATCGGCTTTTGTGCTACGGCATAGTCTGCAATGCTGCTGCTGCTGCTGCTGCT 684
 Db 541 TTTGATCGGCTTTTGTGCTACGGCATAGTCTGCAATGCTGCTGCTGCTGCTGCTGCT 600
 QY 585 GGTCAATTTGCTGCTTATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
 Db 601 GGTCAATTTGCTGCTTATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 745 CATGAGACAGGCAACACAGCCCGAGCCAGTCCATCCGACCATCTCTAGTGTGTG 804
 Db 661 CATGAGACAGGCAACACAGCCCGAGCCAGTCCATCCGACCATCTCTAGTGTGTG 720
 QY 805 CCTCTTACCTCTGTTTGTGCTTCCATATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 864
 Db 721 CCTCTTACCTCTGTTTGTGCTTCCATATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 865 CTTTCTGCTTCTCAGGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
 Db 781 CTTTCTGCTTCTCAGGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 925 GAGGCTCTG 934
 Db 841 GAGGCTCTG 850

RESULT 15
 ADO30397
 ID ADO30397 standard; cDNA; 906 BP.
 XX

AC ADO30397;
 XX 29-JUL-2004 (first entry)
 DT Mouse GPCR P2Y3L polynucleotide, SEQ ID NO:1500.
 DE
 XX
 XX
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antiarrhythmic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; gene; ss.
 XX
 OS Mus musculus.
 XX WO2004040000-A2.
 XX 13-MAY-2004.
 XX
 XX 09-SEP-2003; 2003WO-US028226.
 XX
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 XX (PRIM-) PRIMAL INC.
 XX
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX
 XX WPI; 2004-390329/36.
 DR P-PSDB; ADO30396.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 1500; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia;
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid
 CC AIDS); bone and joint disorders (e.g., osteoporosis); metabolic or nutritive disorders (e.g.,
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,

CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences.

XX
SQ Sequence 906 BP; 173 A; 276 C; 216 G; 241 T; 0 U; 0 Other;

Query Match 56.0%; Score 606.2; DB 12; Length 906;
Best Local Similarity 80.9%; Pred. No. 4.1e-155;
Matches 732; Conservative 0; Mismatches 168; Indels 5; Gaps 2;

Qy 85 ATGGAGAAGGTGGACATGATATACATACAGGAACAGAGTCTGCGCAGTTCTCAGAGAG 144
Db 1 ATGGAGAAGGTAGATATGATGCTCAAGAGGTGCTGGCGCCCTGCCACTTCTCAGAGAG 60

Qy 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 204
Db 61 TACAAGCAAGTCTACCTATCATTAACCTACAGTCTCATCTTTATGCTAGGGATGCCCTC 120

Qy 205 AATGGCACTCTGTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACACC 264
Db 121 AATGGGGCTCTCTATGGCTCTCTGTGTGCAACCAAGCGCTGGAGCTGTGCCACATC 180

Qy 265 TATCTGGTGAACCTGATGTGGCGGACCTCTTTATGTGCTA---TTGCCCTTCTCTCATC 321
Db 181 TACCTGATGAACCTGTGGTGGCTGACCTCTTTATGTAGAGCTGCCCTTGTCTCATC 240

Qy 322 ATCACTTACTCACTAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCAC 381
Db 241 ATCACTTACGGGTGGGTGACACCTGGCTCTTTGGGGAGATGCTGTGCAGTTGGTGGG 300

Qy 382 TTCTGTTCATATCAACCTTTAGGGCAGATCTGCTGTGCTGACCTGCACTCTGTGCAC 441
Db 301 TTCTGTTCATCAACCAACCTCTACAGCAGATCTGCTGTGACCTGCACTCTCTACAC 360

Qy 442 CAGTTCTAGTGTGTCGCCACCACTGTGTGCTGCTGCCCTACCGGACCCCGAGGCATGCC 501
Db 361 CGTTTCTTAGAGTGTGCCACCTCTGAGCTCACTGTCTTACCGGACTCACCGGCACGCC 420

Qy 502 TGGCTGGGCAACGACACACTGGGGCCCTGGTGGTCTCCAGCTGTGCGCCACACTGGCC 561
Db 421 TGGCAGGACGCTGCTGCGCACCTGGACCCCTGGTAGTTCTCCAAATTGCTGCCGACTCTGGTC 480

Qy 562 TTCTCCACACGGACTACATCAATGGCCAGATGATGCTGATGACATGACAGCCCAAGAG 621
Db 481 TTCTCCACACAGACTATGTAATGGCCAGTATGCTGATGACAGCCAGCCCGGAG 540

Qy 622 AATTTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGGCTT--TCTTTCCC 679
Db 541 CAGTTTGATCATTTCTTCGCCCTACAGCATAGTACTGACGTTATCTGGGTTTGTCTTCCC 600

Qy 680 TCCTTGGTCAATTTGGTGTGCTATTCATGATGCTCAGGAGCTGATCAAGCCAGAGGAG 739
Db 601 TCCTTGTATCATTTCTGGTGTGCTCTCTGATGCTTAGGAGCCCTGCAAAATCCAGTGGAG 660

Qy 740 AACCTCATAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACCATCCTACTGGTG 799
Db 561 GACCTCCCAACGACAGGCCACACAGCCCGTCCCAAGTCTATTCCGACCATCCTCTGGTG 720

Qy 800 TGTGGCTCTTCAACCTCTGTTTTGTGGCCCTTCCATATCACTGCTCTCTTCTACTCACC 859
Db 721 TGTGGCTCTTTCACACTCTGTTTTGTGGCCCTTCCACATTTGCCGATTTCTTCTACTTATC 780

Qy 860 ATCTGCTTTCGCTTTCTCAGGACTGCCAGCTCTTGTATGGCAGCAGTGTGGCCCTACAAG 919
Db 781 ATCCGCTTTCCTGAAGTCAAGACTTGCAGCTCTTTGGGAGCCAGCATGGCCCTACAAG 840

Qy 920 ATATGGAGCCCTCTGGTGAAGTGTGAGCAGTGCCTCAACCCAGTCTCTGTACTTTCTTCA 979
Db 841 GTCTGTAGGCTCTGGTAAGCATGAGCAGTGCCTCAATCCAGTCTCTGTACTTCTTGTCA 900

Qy 980 AGGGG 984
Db 901 CAGGG 905

Search completed: November 10, 2004, 09:24:28
Job time : 608 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 10, 2004, 09:24:31 ; Search time 596 Seconds
(without alignments)
3170.791 Million cell updates/sec

Title: US-10-763-972-2

Perfect score: 1936

Sequence: 1 MSLILLPSRSGSGSRGAL.....QNKLGHPAGKRCPLNRS 360

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_23Sep04 -QMT=fastap -SUFFIX=ring -NIMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10763972@cgn 1 1 470 @runat_04112004_093313_8778 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1936	100.0	1082	6	Abq76000 Human GPC
2	1936	100.0	1156	10	Adb99267 Human P2Y
3	1936	100.0	1334	10	Adc86166 Human GPC
4	1936	100.0	3143	6	Aas17746 Human GPC
5	1898	98.0	1063	6	Aas98135 Human DNA
6	1896	97.9	1108	6	Adi16629 Human NOV

7	1896	97.9	1108	12	ADN42283	Adn42283 Human cDN
8	1798	92.9	1002	4	AH73516	Ah73516 Human G p
9	1792	92.6	1017	10	ADC25999	Adc25999 Human pur
10	1792	92.6	1017	10	AA61648	Adc61648 Human GPC
11	1785	92.2	1020	6	AEQ79300	Abq79300 Human GPC
12	1785	92.2	1076	6	AA29667	Adc29667 Human G-p
13	1785	92.2	1076	12	ADO30395	Adc30395 Human GPC
14	1541	79.6	850	6	AAS17747	Aas17747 Human P2Y
15	1063.5	54.9	906	12	ADO30397	Adc30397 Mouse GPC
16	921	47.6	510	4	AAS0975	Ahs0975 Human ngp
17	921	47.6	510	6	ABS70208	Abs70208 DNA enco
18	732	37.8	681	4	AAS30774	Aas30774 Human cDN
19	681	35.2	585	4	AAS30783	Aas30783 Human cDN
20	495	25.6	1163	12	ADP49190	Adp49190 Chick P2Y
21	460.5	23.8	1086	12	ADO30308	Adc30308 Mouse GPC
22	453	23.4	1163	4	AA04981	Aa04981 Human pur
23	446.5	23.1	1651	10	ADK40462	Adk40462 Human pyr
24	446	23.0	1177	10	ADB53313	Adb53313 Primary r
25	445.5	23.0	1428	12	ADP21381	Adp21381 Gene P2RY
26	445.5	23.0	1429	2	AAT74321	Aat74321 Human P2Y
27	445.5	23.0	1429	10	ACA56470	Aca56470 Human sig
28	445.5	23.0	1429	12	ADI56266	Adi56266 Human pol
29	445.5	23.0	1429	12	ADP49192	Adp49192 Human P2Y
30	442.5	22.9	1098	8	ABZ42771	Abz42771 Human pyr
31	442.5	22.9	1098	12	ADO30018	Adc30018 Human GPC
32	442	22.8	1134	12	ADO30017	Adc30017 Human GPC
33	442	22.8	2025	4	AA04980	Aa04980 Human pur
34	442	22.8	2025	6	ABZ35611	Abz35611 Human Gen
35	442	22.8	2025	8	ABZ42713	Abz42713 Human pur
36	442	22.8	2025	10	ACA56884	Aca56884 Human sig
37	442	22.8	2025	12	ADI56680	Adi56680 Human pol
38	442	22.8	2025	12	ADP49188	Adp49188 Human P2Y
39	440	22.7	2118	6	ABZ35320	Abz35320 Human gen
40	436	22.5	1922	10	ABT42366	Abt42366 Toxicity
41	435	22.5	2547	12	ADP21380	Adp21380 Gene P2RY
42	420.5	21.7	984	2	AAT18367	Aat18367 Mouse pan
43	420.5	21.7	987	12	ADO30309	Adc30309 Mouse GPC
44	420.5	21.7	1881	10	ADC37338	Adc37338 Nuclear f
45	416	21.5	1842	2	AAQ88134	Aaq88134 Human P20

ALIGNMENTS

RESULT 1

ABQ76000

ID ABQ76000 standard; DNA; 1082 BP.

XX

AC ABQ76000;

XX 17-OCT-2002 (first entry)

XX Human GPCR designated PFI-020 encoding sequence.

XX Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
KW disorder; PFI-020; gene; ds.
XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1080

FT /*tag= a

FT /partial

FT /product= "GPCR designated PFI-020"

FT /note= "no stop codon given"

XX EP1215214-A1.

XX 19-JUN-2002.

XX 04-DEC-2001; 2001EP-00310137.

XX 18-DEC-2000; 2000GB-00030855.

PR

DR WPI; 2003-364675/35.
 DR P-PSDB; ADB99264.
 XX
 PT New human gene P2Y2L1 and encoded G protein-coupled receptor, useful for
 PT treatment and diagnosis of receptor-associated diseases and for drug
 PT screening.
 XX
 PS Disclosure; Page 4; 5pp; German.
 XX
 CC This invention describes the human P2Y2L1 gene and its 5' - and 3' -
 CC untranslated regions, located on chromosome 3 which is a novel G protein-
 CC coupled receptor (GPCR). The protein encoded by P2Y2L1 is expressed in
 CC blood cells, testis and embryonal kidney cells and contains potential
 CC sites for phosphorylation by protein kinase C and casein kinase II. It is
 CC a member of the Class A rhodopsin-like sub-family of G protein-coupled
 CC receptors and it probably a nucleoside/nucleotide receptor that mediates
 CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2L1 and
 CC antibodies directed against the encoded protein are useful in diagnosis
 CC and treatment (including gene therapy) of diseases associated with
 CC abnormal levels of P2Y2L1 expression, in screening assays for modulators,
 CC potential therapeutic agents, and to produce transgenic animals, e.g. for
 CC identifying diseases associated with abnormal expression of P2Y2L1. This
 CC sequence represents the P2Y2L1 gene described in the disclosure of the
 CC invention.
 XX
 SQ Sequence 1156 BP; 243 A; 335 C; 295 G; 283 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,2e-176 Length: 1156
 Score: 1936.00 Matches: 360
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-763-972-2 (1-360) x ADB99267 (1-1156)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 DB 21 ATCTGTCCATTTTGTCTCTCCAGGGAGAGCAGAGGGAGCGTGTGGAGCTGTG 80
 QY 21 LeuLeuGluAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
 DB 81 CTCCTGGAGGAGCCCTCCCGGAGCATGGAGAGGTGGACATGAATACATCAGAGAACAA 140
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 DB 141 GGTCTGTCCAGTCTTCAGAGAGTACAGCAAGTCTACTCTCCCTGGCCCTACAGTATC 200
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTrpGlyGlnThr 80
 DB 201 ATCTTTATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTCTCTGGGGCCAAACC 260
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 DB 261 AAGCGCTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGTGGCCGACCTGCTTTAT 320
 QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGlu 120
 DB 321 GTGCTATTGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 380
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 DB 381 CTGCTCTGCAAGCTGGTGGCACTTCTCTGTATATCAACCTTTACGGCAGCATCTCGCTG 440
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 DB 441 CTGACCTGCATCTCTGTGCCACCACTCTAGGTGTGTGCCACCACTGTGTGGTGGCC 500
 QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValLeu 180
 DB 501 TACGGACCGGACGATGCTGGCTGGGACCAACAGCACCTGGGCGCTGTGGTCTC 560

QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 DB 561 CAGCTGTGTGCCACACTGGGCTTCTCCACACGAGACTACATCAATGATGCCAGATGATCTGG 620
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 DB 621 TATGACATGACCAAGAGATTTTGTATCGGCTTTTGTCTACGGCATAGTTCTGACA 680
 QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 DB 681 TTGTCTGGCTTCTTTCCTCCCTTGGTCATTTTGTGTGTCTATTCACTGATGGTCAGAG 740
 QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 DB 741 CCTGATCAGCCAGGAGGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCAT 800
 QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 DB 801 CCGGACCATCTACTGTGTGTGGCTCTTCACTCTGTGTGTGTGGCTCTCCATATCAC 860
 QY 281 SerLeuLeuLeuProHisHisLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 861 TCGTCTCTTCTACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 920
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 DB 921 AGCCAGTGTGGCTTACAAGATATGAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 980
 QY 321 SerProValLeuSerPheLysGlyGlyLysAsnArgValArgLeuLeuGlnLysLeuArg 340
 DB 981 AGTCTGTACTTCTTTCAGAGGGGGCAAAATAGATGAGCTCTCTCCAGAAACTGAGG 1040
 QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysCysProGlyLeuAsnArgSer 360
 DB 1041 CAGAACAGTTGGGTGAGCATCCAGCTGGGAGGAAGAGATGCCCGGGTTGACAGATCT 1100

RESULT 3
 ADC86166
 ID ADC86166 standard; DNA; 1334 BP.
 XX
 AC ADC86166;
 XX
 DT 01-JAN-2004 (first entry)
 DE Human GPCR gene SEQ ID NO:619.
 XX
 KW ds; Gene; human; GPCR;
 XX
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 DR WPI; 2003-315783/31.
 DR P-PSDB; ADC86167.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT Guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 1; SEQ ID NO 619; 28pp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC8548-ADC87616 encode GPCR's of the
 CC invention.

XX
 SQ Sequence 1334 BP; 283 A; 368 C; 348 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.48e-176 Length: 1334
 Score: 1936.00 Matches: 360
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

us-10-763-972-2 (1-360) x ADC86166 (1-1334)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 DB 117 ATGCTGTCATTTGCTTCTTCAGGGGAAGCAGAGCGGAGCGCTGCGAGCTCTG 176
 QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
 DB 177 CTCCTGAGGGAGCCTCCGGGACATGGAGAGGTGGACATGAATACATCACAGGAACA 236
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 DB 237 GGTCTCTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCCTACATATC 296
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrPheSerIleGlyGlnThr 80
 DB 297 ATCTTTATCTAGGCTGCCACTAATGGACATGCTCTGTGGACATCTCTGGGCCCAACC 356
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 DB 357 AAGCGCTGGAGCTGTGCCACCATCTCTGTGTGAACCTGATGTGTGGCCGACCTGCTTTAT 416
 QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspAspArgTrpPheGlyGlu 120
 DB 417 GTGCTATGGCTTCTCTATCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 476
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 DB 477 CTGCTCTGCAAGCTGTGGTGCATCTCTCTATATCAACCTTTACGGCAGCATCTCTGCTG 536
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 DB 537 CTGACCTGCATCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCATCTGTGTGGTGGCC 596
 QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
 DB 597 TACCGGACCGCAGGCATGCTGCTGGGCACCGACACCATCTGGCCCTGTGTGGTCTCTC 656
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 DB 657 CAGCTGTGCCCATCTGTGGCTTCTCCACACGAGTATCATCAATGCCAGATGATCTGTG 716
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 DB 717 TATGACATGACCGCAAGAGATTTTGATCGCTTTTGGCTACCGCATAGTCTTGACA 776
 QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 DB 777 TTGCTGTGGCTTCTTTCCCTCTGTGTGATTTTGTGTGCTATTCACTGATGTCAGGAG 836
 QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 DB 837 CCTGATCAACCCAGAGGAGAACCTCATGAGGACAGGACGACACAGCCCGGAGCCAGTCCAT 896

QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 DB 897 CGGACCATCTACTGTGTGTGGCTTTCACCTCTGTTTGTGGCTTCCATATCAC 956
 QY 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 DB 957 TCGTCTCTTCTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGC 1016
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 DB 1017 AGCCAGTGTGCCCTACAGATATGGAGGCTCTGCTGAGTGTGAGCAGCTCCCAACCC 1076
 QY 321 SerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeuArg 340
 DB 1077 AGTCTGTACTTCTTCAAGGGGGCAAAAATAGAGTCAGGCTCTCCAGAACTCAGG 1136
 QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
 DB 1137 CAGAACAGTTGGGTGAGCATCCAGCTGGGAGGAGAGATGCCCAGGGTTGAACAGATCT 1196

RESULT 4
 AAS17746
 ID AAS17746 standard; DNA; 3143 BP.
 XX AAS17746;
 DT 26-FEB-2002 (first entry)
 XX
 DE Human genomic clone for P2Y-like G protein-coupled receptor.
 XX
 KW Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;
 KW chronic obstructive pulmonary disease; nervous system disease;
 KW Parkinson's disease; multiple sclerosis; dementia; stroke;
 KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
 KW bacterial infection; fungal infection; protozoan infection;
 KW viral infection; pain; cancer; anorexia; bulimia; asthma;
 KW acute heart failure; hypotension; hypertension; osteoporosis; diabetes;
 KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; delirium; severe mental retardation; dyskinesia.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 520..2498
 FT /*tag= a
 FT /product= "P2Y-like GPCR"
 XX
 PN WO200185764-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-EP005244.
 XX
 PR 11-MAY-2000; 2000US-0203582P.
 PR 21-FEB-2001; 2001US-0269857P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI; 2002-075242/10.
 DR P-PSDB; AAU11251.
 XX
 PT New polynucleotides for producing P2Y-like G protein-coupled receptors
 PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-
 PT like GPCR, especially useful for treating pain, cancer or neurological
 PT disorders.
 XX
 PS Disclosure; Fig 1; 114pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a P2Y-like G
 CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or

CC allele, a host cell containing an expression vector comprising the
 CC polynucleotide and screening for agents that regulate the GPCR activity.
 CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide,
 CC which may be employed for screening agents that inhibit or regulate human
 CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is
 CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly
 CC COPD (chronic obstructive pulmonary disease), peripheral or central
 CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,
 CC dementia, stroke, Alzheimer's disease and many other diseases and
 CC disorders listed in the specification), benign prostatic hyperplasia or
 CC urinary incontinence. A pharmaceutical composition containing the
 CC modulators and/or regulators of P2Y-like GPCR is useful for modulating
 CC the activity of a P2Y-like GPCR. In particular, these are useful for
 CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,
 CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,
 CC acute heart failure, hypotension, hypertension, osteoporosis, diabetes,
 CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,
 CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic
 CC depression, delirium, severe mental retardation or dyskinesias). The
 CC present sequence is a genomic clone encoding the P2Y-like GPCR of the
 CC invention

SQ Sequence 3143 BP; 818 A; 771 C; 726 G; 828 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,07e-176 Length: 3143
 Score: 1936.00 Matches: 360
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-763-972-2 (1-360) x AAS17746 (1-3143)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 Db 436 ATGCTCTCCATTTTGTCTCTCCAGGGAGACAGAGAGCGGCGCTGTGAGCTCTG 495
 QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGlu 40
 Db 496 CTCCTGGAGGAGCCCTCCCGGACATGGAGAGGTGGACATGATATACATCAGAGAACAA 555
 QY 41 GlyLeuCysGlnPheSerGluLysValGlnValTyrLeuSerLeuAlaTyrSerile 60
 Db 556 GGTCTCTGCAGTTCTTCAGAGAGATACAGCAGAGTCTACTCTCTCCGCGCTACAGTATC 615
 QY 61 IlePheIleLeuGlyLeuProLeuAenGlyThrValLeuTrpPheSerTrpGlyGlnThr 80
 Db 616 ATCTTTATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTCTCTGGGGCCAAACC 675
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuTyr 100
 Db 676 AAGCGCTGGAGCTGCCACCACTATCTGGTGAACCTGATGTGGCCGACCTGCTTTAT 735
 QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspArgTrpProPheGlyGlu 120
 Db 736 GTGCTATTGCCCTTCTCATCTACCTACTCCTACATGACAGGTGGCCCTTCGGGGAG 795
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 Db 796 CTGCTCTGCAAGCTGTGCACTTCTCTTATATCAACCTTACGGCAGCATCTCTGCTG 855
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 Db 856 CTGACCTGCATCTCTGTGCACCAAGTCTTAGGTGTGTGCCACCCACTGTGTGCTGCC 915
 QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
 Db 916 TACCGGACCGCAGGATGCTGCTGGCCAGTCCAGTGTGTGCCACCCACTGTGTGCTGCC 975
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 Db 976 CAGTGTGCCACCTAGGCTTCTCCACACGAGATATCAATATGCGCAGATGATCTGG 1035

QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 Db 1036 TATGACATGACACGACCAAGAAATTTGATCGGCTTTTTCCTACGCAATGTCGACA 1095
 QY 221 LeuSerGlyPheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 Db 1096 TTGCTCGCTTCTTCTCCCTCTTCTGGTCATTTTGGTGTGCTATTCACTGATGTCAGAG 1155
 QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 Db 1156 CCTGATCAAGCAGGAGGAACCTCATGAGGACAGGACACAGCCCGCCAGGTCAT 1215
 QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 Db 1216 CCGACCATCTACTGTGTGTGGCTCTTCACTCTCTGTTTGTGGCTTCCATATCAC 1275
 QY 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 Db 1276 TCGCTCTCTTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGC 1335
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 Db 1336 AGCCAGTGTGGCTTACAGATATGAGGCTCTGTGTGAGTGTGAGCAGCTGCCTCAACC 1395
 QY 321 SerProValLeuSerPheLysGlyGlyLysAsnArgValArgLeuLeuGlnLysLeuArg 340
 Db 1396 AGTCTCTGCTACTTCTTCAAGGGGGCAAAATAGAGTACAGGCTCCTCCAGAACTGAGG 1455
 QY 341 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
 Db 1456 CAGAACAGTTGGTGTGAGCATCCAGCTGGAGAGAGATGCCAGGGTTGACAGATCT 1515
 RESULT 5
 ID AAS98135 standard; DNA; 1063 BP.
 AC AAS98135;
 XX 12-MAR-2002 (first entry)
 DE Human DNA for potential G protein-coupled receptor #92.
 KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
 KW Alzheimer's disease; ankyrotrophic lateral sclerosis; asthma;
 KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
 KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
 KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
 KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
 KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
 KW tuberculosis; cognition disorder; memory disorder; anorexia;
 KW hormonal release disorder; cardiovascular activity disorder;
 KW pain perception disorder; obesity; diabetes; obesity; diabetes;
 KW hyperlipidaemia; stroke; gene therapy.
 OS Homo sapiens.
 FN WO200185791-A1.
 XX 15-NOV-2001.
 PD 11-MAY-2001; 2001WO-US015332.
 PF 11-MAY-2001; 2000US-0203217P.
 PR 18-MAY-2001; 2000US-0205945P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA Brown JP, Miller M, Burmer G, Fabre-Suver C, Pritchard D;
 XX WPI; 2002-066595/09.
 DR Novel G protein-coupled receptor polypeptides including galanin receptor
 XX

PT polypeptides useful for identifying modulators that are useful for
 PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
 XX stroke.

PS Claim 2; Page 98; 144pp; English.

XX The invention relates to an isolated polypeptide encoded by a nucleic
 CC acid molecule that is at least 80% identical to the G protein-coupled
 CC (GPCR) polynucleotides included in the specification. Also included are
 CC probes based on the GPCR sequences (including antisense probes), a host
 CC cell comprising an expression vector comprising the GPCR sequence,
 CC antibodies raised against the polypeptides, and methods of identifying
 CC modulators of the polypeptides. The polypeptides are useful for
 CC identifying modulator compounds which function as modulators, activators,
 CC repressors, agonists or antagonists of the novel GPCR polypeptides
 CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as
 CC described above can be used to detect the presence of the polypeptides
 CC and nucleic acids and are used to diagnose a variety of diseases or
 CC disorders in which GPCRs are involved e.g., Alzheimer's disease,
 CC amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell
 CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
 CC obstructive pulmonary disease, Crohn's disease, depression, epilepsy,
 CC macular degeneration, lymphoma, melanoma, multiple sclerosis,
 CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid
 CC arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other
 CC diseases listed in the specification. The probes and antibodies are also
 CC useful for diagnosing cognition and memory disorders, anorexia, hormonal
 CC release disorders, cardiovascular activity disorders, pain perception
 CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
 CC that decrease or increase the expression of galanin receptor (GAL4) can
 CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
 CC nucleic acid is useful for treating the above mentioned disorders by gene
 CC therapy techniques. The present sequence is a novel GPCR polynucleotide
 CC of the invention

XX SQ Sequence 1063 BP; 216 A; 315 C; 272 G; 260 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.92e-173 Length: 1063
 Score: 1898.00 Matches: 354
 Percent Similarity: 99.72% Conservatives: 0
 Best Local Similarity: 99.72% Mismatches: 0
 Query Match: 98.04% Indels: 1
 DB: 6 Gaps: 0

US-10-763-972-2 (1-360) x AAS98135 (1-1063)

QY 7 ProSerHrglySerArgSerGlySerArgArgGlyAlaLeuLeuGlyAlaSer 26
 DB 1 CCTTCCAGGGGAAGCAGAGCGGAGCCGCTGCTGGAGCTCTGCTGGAGGAGGCTCC 60
 QY 27 ArgAspMetGluLysValAspMetAsnThrSerGlnGlnGlnGlyLeuCysGlnPheSer 46
 DB 61 CGGACATGAGAGGAGTGACATGATACATACAGGACAGAGTCTCTGCCAGTTCTCA 120
 QY 47 GluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIleIlePheLeuGlyLeu 66
 DB 121 GAGAAGTACAGCAAGTCTACCTCTCCCTGGCCATCATCATCATCTTATCTTCCTAGGGCTG 180
 QY 67 ProLeuAsnGlyThrValLeuTyrPheSerTrpGlyGlnThrLysArgTrpSerCysAla 86
 DB 181 CCATAAATGGCACTGCTCTGGCACTCTCTGGGCGCAACCAAGCGCTGGAGCTGTGCC 240
 QY 87 ThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeuLeuPropheLeu 106
 DB 241 ACCACCTATCTGGTGAACCTGATGGTGGCCGACCTGCTTATGTGCTATTCCTTCCTC 300
 QY 107 IleIleThrTyrSerLeuAspAspArgTrpPheGlyGlnLeuLeuCysLysLeuVal 126
 DB 301 ATATCATCTACTACTAGATGACAGTGCGCCCTTCGGGAGCTGCTCTGCAAGCTGGTG 360
 QY 127 HisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerVal 146

DB 361 CACTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTGACCTGCATCTCTGTG 420
 QY 147 HisGlnPheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThrArgArgHis 166
 DB 421 CACCAGTTCTTAGGTGTGTGCCACCCACTGTGTGTGCTGCCCTACCGGACCGGAGCAT 480
 QY 167 AlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeuLeuProThrLeu 186
 DB 481 GCCTGGCTGGGCACAGCAGCACCCTGGGCCCTGGTGTCTCTCCAGCTGCTGCCCACTG 540
 QY 187 AlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGln 206
 DB 541 GCCTTCTCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCCAGCAA 600
 QY 207 GluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeuSer 226
 DB 601 GAGAATTTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTCTGGCTTTCTTTCC 660
 QY 227 LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgGly 246
 DB 661 CTCTTGGTCACTTTTGGTGTGCTATTCTCTGATGGTCAGAGGCTGATCAAGCCAGGGA 720
 QY 247 GluProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGly 266
 DB 721 CAACCTCATGAGGACAGGCAACACAGCCGAGGCTCCATCCGACCATCTCTACTTGGT 780
 QY 267 ValTrpProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHis 286
 DB 781 GTGTGGCTCTTCACTCTGTTTGTGGCTTCCATATCATCTGCTCTCTTACTCTAC 840
 QY 287 HisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuG 306
 DB 841 CATCTGCTTTCTGCTTCTCAGGACTCCAGCTCTTGTATGGCAGCCAGTGGCTTACA 900
 QY 306 NASpMetGluAlaSerGlyGluCysGluGlnLeuProGlnProSerProValLeuSerPh 326
 DB 901 AGATATGAGGCTCTCTGCTGAGTGTGAGAGCTCCCTCAACCCAGCTCTGCTACTTTCTTT 960
 QY 326 eLysGlyGlyLysAsnArgValArgLeuLeuGlnLysLeuArgGlnAsnLysLeuGlyG 346
 DB 961 CAAGGGGGCAAAATAGATGATGAGTCTCTCCAGAACTCAGGACAGCAAGTTGGGTGA 1020
 QY 346 uHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSer 360
 DB 1021 GCATCCAGCTGGGAGGAGATGCCCGAGGTTGAACAGATCT 1063

RESULT 6
 ADI16629
 ID ADI16629 standard; cDNA; 1108 BP.
 XX AC ADI16629;
 XX DT 15-APR-2004 (first entry)
 XX DE Human NOVX cDNA to treat human pathological conditions SeqID165.
 XX gene; ss; human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytosolic; cardiact; antiinflammatory; immunosuppressive; anorectic;
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
 KW antiaesthetic; nephrotropic; antiarthritic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic;
 KW single nucleotide polymorphism; SNP.
 XX Homo sapiens.
 XX CS
 XX Key Key Location/Qualifiers
 XX variation replace(378,A)
 FT

PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTA K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX
PI Tchernev VT, Spytek KA, Zernhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2004-180039/17.
DR P-PSDB; ADN42284.
XX
PT Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX
PS Claim 9; SEQ ID NO 165; 1309pp; English.
XX
CC The invention relates isolated 162 NOVX polypeptides (NOVX-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (NA) and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
CC modulating the activity of NOVX, treating or preventing a NOVX-associated
CC disorder, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX and treating a pathological state
CC in a mammal comprising administering a polypeptide which is at least 95%
CC identical to NOVX (or fragment). NOVX and NA may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC detecting the presence of NOVX in samples (e.g. by enzyme linked
CC immunosorbent assay (ELISA)). The agents and methods may be used in this
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC and/or atherosclerosis. The present sequence encodes a NOVX protein.
XX
SQ Sequence 1108 BP; 225 A; 321 C; 285 G; 277 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.14e-173 Length: 1108
Score: 1896.00 Matches: 359
Percent Similarity: 99.45% Conservative: 0
Best Local Similarity: 99.45% Mismatches: 1
Query Match: 97.93% Indels: 2
DB: 12 Gaps: 0

US-10-763-972-2 (1-360) x ADN42283 (1-1108)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
Db 12 ATGCTGCCATTTTTCCTCCAGGGGAAGCAGAGCGGAGCGCTCGTGAGCTCTG 71
QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGlu 40
Db 72 CTCTGGAGGAGGCTCCCGGACATGAGAGGTGGACATGATATCATCACAGGAACA 131
QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60

Db 132 GGTCTCTGCCAGTTCTCAGAGAACTACAAGCAAGTCTACCTCTCCCTGGCTACAGTATC 191
QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThr 80
Db 192 ATCTTTATCTAGGCTGCCACTAAATGGCACTCTTGTGGCACTCTCTGGGGCAAAACC 251
QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
Db 252 AAGGCTGGAGCTGTGCCACCACTATCTGTGTAACCTGTATGGTGGCGAGACTCTTTAT 311
QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu 120
Db 312 GTGCTATTGCCCTTCTCTCATCATCACTACTCATAGATGACAGGTGGCCCTTCGGGAG 371
QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
Db 372 CTGCTCTGCAAGCTGGTGCACTCTCTGTATATCAACCTTTACGGCAGCATCCTGCTG 431
QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
Db 432 CTGACCTGCATCTCTGTGCACCACTTCTTAGTGTGTGCCACCCACTGTGTCTCGTCCC 491
QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
Db 492 TACCGGACCCGACGACATGCTGGTGGCAACCAACCACTGGGCTGGTGGTCTCTC 551
QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
Db 552 CAGCTGTGCTGCCACACTGGCCTTCTCCACAGGACTACATCAATGGCCAGATGATCTGG 611
QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
Db 612 TATGACATGACCAAGAGAAATTTGATCGGCTTTTGCTACGGCATAGTTCTGACA 671
QY 221 LeuSerGlyPheLeuSerLeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
Db 672 TTGCTGGCTTCTTCTTCCCTCTGGTCAATTTGGTGTA-TTCACCTGATGGTCAGAG 730
QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
Db 731 CCTGATCAAGCCAGGAGAGACCTCATGAGGACAGGACACACAGCCGAGCCAGTCCAT 790
QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
Db 791 CCGGACCATCTACTGTGTGTGGCTTTCACCTCTCTGTGTCCTTTCATATATCAC 850
QY 281 SerLeuLeuLeuProHisHisIleLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
Db 851 TGGCTCTCTTACCTTCACTCACTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGCC 910
QY 301 Ser-GlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPr 320
Db 911 AGCCCAAGTGTGGCTTACAAGATATGGAGGCTCTGCTGAGTGTGAGCAGTGCCTCAACC 970
QY 320 OSerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeuAr 340
Db 971 CAGTCTCTTACTTTCTTCAAGGGGGGCAAAATAGACTAGGCTCTCTCCAGAACTCAG 1030
QY 340 GlnAsnLysLeuGlyGluHisProAlaGlyArgLysArgCysProGlyLeuAsnArgSe 360
Db 1031 GCAGAACAAAGTTGGTGAGCATCCAGCTGGGAGGAGAGATGCCCGAGGTTGAACAGATC 1090
QY 360 r 360
Db 1091 T 1091.
RESULT 8
AAH73516
ID AAH73516 standard; DNA; 1002 BP.
XX
XX AAH73516;
DT 25-SEP-2001 (first entry)

XX Human G protein-coupled receptor GPRv71 coding sequence.

XX Human; guanosine triphosphate binding protein-coupled receptor;

KW G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;

KW GPRv47; GPRv51; GPRv72; cancer; liver cirrhosis;

KW Alzheimer's disease; cytostatic; hepatotropic; neotropic;

KW neuroprotective; gene therapy; peptide therapy; ds.

OS Homo sapiens.

XX WO200148188-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-JP009408.

XX 28-DEC-1999; 99JP-00375152.

XX 31-MAR-2000; 2000JP-00101339.

XX (HELI-) HELIX RES INST.

XX Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;

PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;

XX WPI; 2001-425662/45.

DR P-ESDB; AAG64125.

XX New DNA encoding guanosine triphosphate binding protein coupled receptors

PT and their expression products for screening potential anticancer and

PT neotropic drugs and in diagnosis of these diseases.

XX Example 1; Page 142-143; 170pp; Japanese.

XX The invention relates to nine human guanosine triphosphate binding

CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,

CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes

CC encoding them. These genes and proteins and antibodies against the

CC protein are useful in the treatment, prevention, diagnosis and

CC investigation of diseases associated with G protein-coupled receptors,

CC including cancer, cirrhosis of the liver and Alzheimer's disease. The

CC present sequence is a G protein-coupled receptor coding sequence of the

CC invention

XX Sequence 1002 BP; 207 A; 293 C; 249 G; 253 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 1.98e-163 Length: 1002

Score: 1798.00 Matches: 331

Percent Similarity: 99.70% Conservative: 0

Best Local Similarity: 99.70% Mismatches: 1

Query Match: 92.87% Indels: 0

DB: 4 Gaps: 0

US-10-763-972-2 (1-360) x AAH73516 (1-1002)

QY 29 MetGluValAspMetAsnThrSerGlnGluGlnGlyLeuCysGlnPheSerGluLys 48

DB 1 ATGGAGAGGTGGACATGATATACATACAGAGACAGGCTCTGCCAGTCTCAGAGAG 60

QY 49 TyrIysGlnValTyrLeuSerLeuAlaTyrSerIlePheIleLeuGlyLeuProLeu 68

DB 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120

QY 69 AsnGlyThrValLeuTyrHisSerTrpGlyGlnThrIleArgTrpSerCysAlaThrThr 88

DB 121 AATGGCACTGTCTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACACC 180

QY 89 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeuLeuProPheLeuIleIle 108

DB 181 TATCTGGTGAACCTGATGGTGGCGGACCTCTTATGTGCTATTGCTCTCTCATCATC 240

QY 109 ThrTyrSerLeuAspAspArgTrpProPheGlyGluLeuLeuCysIysLeuValHisPhe 128

DB 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTCAAGCTGGTGCACATTC 300

QY 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148

DB 301 CTGTTCTTATATCAACCTTTAGCGGAGCATCTGCTGCTGACCTCATCTCTGTGCACAG 360

QY 149 PheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThrArgHisAlaTyr 168

DB 361 TTCCTAGGTGTGGCCACCCACTGTGTCGCTGCCCTACCGGACCGGAGCATGCGCTGG 420

QY 169 LeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeuLeuProThrLeuAlaPhe 188

DB 421 CTGGGCACCCAGCACCCCTGGGCGCTGGTGTCTCCAGCTGCTGCCACACTGGCCTTC 480

QY 189 SerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGlnGluAsn 208

DB 481 TCCACACGGACTACATCATGGCCAGATGATCTGGTATGACATGACCCAGCAGAGAT 540

QY 209 PheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPheLeuSerLeu 228

DB 541 TTTGATCGCTTTTGGCTACGGCATAGTCTGACATTTCTGGCTTTCTTTCCCTCCTT 600

QY 229 GlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgGlyGluPro 248

DB 601 GGTCAATTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGGAGACCT 660

QY 249 HisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTrp 268

DB 661 CATGAGGACAGGCAACACAGCCCGAGGTCAGGTCCATCCGGACCATCTACTGTTGTGG 720

QY 269 ProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisIleu 288

DB 721 CCTCTCACCTCTGTTTGTGGCTTCCATATCACTCGCTCTTCACTCCATCATCTG 780

QY 289 LeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMet 308

DB 781 CTTTCTGTTTCTCAGGACTGCGAGCTTTGATGGCAGCCAGTGTGGCTACAGATATG 840

QY 309 GluAlaSerGlyGluCysGluGlnLeuProGlnProSerProValLeuSerPheLysGly 328

DB 841 GAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTTCTTTCTTCAAGGGG 900

QY 329 GlyIysAsnArgValArgLeuLeuGlnIysLeuArgGlnAsnLysLeuGlyGluHisPro 348

DB 901 GCCTAAATAGATCAGGCTCTCCAGAACTGAGGAGAGACAAAGTTGGTGGTGCATCCA 960

QY 349 AlaGlyArgLysArgCysProGlyLeuAsnArgSer 360

DB 961 GCTGGAGGAAGAGATGCCAGGTTGAACAGATCT 996

RESULT 9

ADC25999

ID ADC25999 standard; DNA; 1017 BP.

XX

AC ADC25999;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human purinergic receptor P2Y-related GPCRv6 DNA.

XX

KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;

KW anorectic; cardiant; hypotensive; osteopathic; antianginal;

KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;

KW neotropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;

KW GPCR; viral; fungal; bacterial infection; immune-related disorder;

KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;

KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;

KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;

KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;

XX human; GPCRv6; purinergic receptor P2Y; ds; gene.

OS Homo sapiens.

```

XX Key
FH CDS
FT Location/Qualifiers
FT 1..1017
FT /product= "Human purinergic receptor P2Y-related GPCR $\alpha$ 6
FT protein - both "original" and "alternative" versions"
FT /transl_except= (pos:184..186, aa:Pro)
FT /transl_except= (pos:727..729, aa:Xaa)
FT /transl_except= (pos:808..810, aa:Pro)
FT /note= "Xaa = Unknown; translation exceptions at 184 and
FT 727 are present within "original" protein CDS whilst that
FT at 808 is present within the "alternative" protein CDS"
FT US2003088080-A1.
XX
XX 08-MAY-2003.
XX
XX 21-JUN-2001; 2001US-00885453.
XX
XX 20-JUN-2000; 2000US-0212908P.
XX 05-DEC-2000; 2000EP-00870289.
XX
XX (COMM/) COMMUNI D.
XX (LANV/) LANNOY V.
XX (GOVA/) GOVAERTS C.
XX (PARM/) PARMENTIER M.
XX (DETH/) DETHEUX M.
XX
XX Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;
XX WPI; 2003-657983/62.
XX P-PSDB; ADC26000, ADC26009.
XX
XX New human G-protein coupled receptor, useful for treating receptor-
XX mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
XX acute heart failure, osteoporosis, stroke, ulcer, allergy, or
XX neurological disorders.
XX
XX Example 3; Page 15-16; 24pp; English.
XX
XX The invention relates to a novel G-protein coupled receptor (GPCR). The
XX receptor, polynucleotide, agonist, reverse agonist and antagonist of the
XX invention may be useful for treating receptor-mediated disorders
XX including viral, fungal or bacterial infections, immune-related disorders
XX such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
XX hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
XX ulcer and allergy, as well as psychiatric and neurological disorders such
XX as schizophrenia and dementia, degenerative diseases such as Parkinson's
XX disease and Alzheimer's disease and dyskinesias such as Huntington's
XX disease. The current sequence is that of the human purinergic receptor
XX P2Y-related GPCR $\alpha$ 6 DNA of the invention.
XX
XX SQ Sequence 1017 BP; 200 A; 306 C; 252 G; 259 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 7.68e-163 Length: 1017
XX Score: 1792.00 Matches: 338
XX Percent Similarity: 99.71% Conservative: 0
XX Best Local Similarity: 99.71% Mismatches: 1
XX Query Watch: 92.56% Indels: 1
XX DB: 10 Gaps: 0
XX
XX US-10-763-972-2 (1-360) x ADC25999 (1-1017)
XX
XX Qy 1 MetLeuSerLeuLeuLeuProSerArgGlySerArgSerGlySerArgArgGlyAlaLeu 20
XX Db 1 ATGCTGTCCATTTTTCCTTCCTCAGGGGAGCAGCAGCGGAGCGCGCTGCTGGAGCTCTG 60
XX
XX Qy 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40
XX Db 61 CTCTCTGAGGAGGAGCTCCCGGACATGAGAGCTGGACATGATATACATCAGAGGACAA 120
XX
XX Qy 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60

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Db 121 GGTCTCTGCCAGTTCTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCGCTACAGTATC 180
Qy 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTrpHisSerTrpGlyGlnThr 80
Db 181 ATCTTTATCTTAGGGCTGCCACTAAATGGCACTCTCTGTGGCACTCTCTGGGGCAAAACC 240
Qy 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
Db 241 AAGCGCTGGAGCTGTGCCACCACTATCTGTGTAACTGATGTGTGGCGGACCTGCTTAT 300
Qy 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspArgTrpPropheGlyGlu 120
Db 301 GTGCTATTGGCCCTTCTCCATCATCACCTACTACTAGATGACAGTGCCCTTTCGGGAG 360
Qy 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
Db 361 CTGCTCTGCAAGCTGGTGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCCTGCTG 420
Qy 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
Db 421 CTGACCTGCATCTCTGTGCACCACTTCTTAGTGCTGTGCCACCACTGTGTCTGCTGCC 480
Qy 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
Db 481 TACCGGACCCGAGCATGCTGTGGTGGGACACGACCACTCTGGGCCCTGGTGGTCTCTC 540
Qy 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
Db 541 CAGCTGTCTGCCACACTTGGCCCTTCTCCACACGAGCTACATCAATGCGCAGATGATCTGG 600
Qy 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
Db 601 TATGACATGACGACGAGCAAGAAATTTGATCGGCTTTTGTCTACGGCATAGTCTTGACA 660
Qy 221 LeuSerGlyPheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
Db 661 TTGCTGTGGCTTTT-TCCTCTCTTGGTCAATTTGGTGTGCTATTCACTGATGGTCAGGAG 719
Qy 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
Db 720 CTTGATCAAGCAGCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGGCTCCAT 779
Qy 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
Db 780 CCGGACCACTCTCTACTGGTGTGTGGCTCTTCACTCTCTGTTTGTGGCCCTTCCATATC 839
Qy 281 SerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
Db 840 TCGCTCTCTTCACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 899
Qy 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
Db 900 AGCCAGTGTGGCTTCAAGATATGAGGCGCTCTGTGTGAGTGTGACAGCTGCTTCAACCC 959
Qy 321 SerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeu 339
Db 960 AGTCTCTGTACTTCTTTCAGGGGGGCAAAATAAGTAGTCAAGTCAAGTCTCTCCAGAACTG 1016
XX
XX RESULT 10
XX AAD61648
XX ID AAD61648 standard; DNA; 1017 BP.
XX AC AAD61648;
XX XX
XX DT 15-JAN-2004 (first entry)
XX DE Human GPCR $\alpha$ 6 DNA.
XX
XX Human; G-protein coupled receptor; GPCR; infection; neoplastic process;
XX inflammation; myocardial infarction; atherosclerosis; angina pectoris;
XX hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;
XX diabetes; cancer; virucide; analgesic; cardiant; gene; ds.

```

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1017
 XX FT /*tag= a
 XX FT /product= "Human GPCR protein"
 XX PN US2003108986-A1.
 XX PD 12-JUN-2003.
 XX PF 20-FEB-2002; 2002US-00079384.
 XX PR 21-JUN-2001; 2001US-00885453.
 XX FA (EURO-) EUROSCREEN SA.
 XX PI Communi D, Lannoy V, Brezillon S, Dethaux M, Parmentier M;
 XX PI Govaerts C;
 XX DR WPI; 2003-810852/76.
 XX DR P-ESDB; ABW00804.
 XX PT Novel G-protein coupled receptor useful for treating viral infections,
 XX PT bacterial infections, fungal infections, cancer, diabetes, hypertension,
 XX PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.
 XX PS Claim 5; Fig 4; Opp; English.
 XX CC The present invention relates to novel G-protein coupled receptors
 CC (GPCRs) and the nucleic acids encoding them. The invention is useful for
 CC treating viral, bacterial and fungal infections, inflammatory and
 CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,
 CC angina pectoris, myocardial infarction and atherosclerosis. The present
 XX sequence is human G-protein coupled receptor (GPCR) DNA
 SQ Sequence 1017 BP; 200 A; 306 C; 252 G; 259 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7 68e-163 Length: 1017
 Score: 1792.00 Matches: 338
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 92.56% Indels: 1
 DB: 10 Gaps: 0
 US-10-763-972-2 (1-360) x AAD61648 (1-1017)
 QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgArgGlyAlaLeu 20
 Db 1 ATGCTGTCATTTTGTCTCTCCAGGGGAAGCAGAGCGGGAGCGCTCGTGGAGCTCTG 60
 QY 21 LeuLeuGluGlyAlaSerArgAspMetGluValAspMetAsnThrSerGlnGluGln 40
 Db 61 CTCCTGGAGGAGCTCCCGGACATGGAAGAGTGGACATGAATACATCACAGGAACAA 120
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 Db 121 GGTCTCTGCCAGTTCTCAGAGAGTACACAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuThrPheSerTrpGlyGlnThr 80
 Db 181 ATCTTTATCTAGGGCTGCCACCACTATCTGTAACCTGATGTGGCCGACCTCTTTAT 240
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 Db 241 AAGCGCTGGAGCTGCGCACCACTATCTGTAACCTGATGTGGCCGACCTCTTTAT 300
 QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspArgTrpPheGlyGlu 120
 Db 301 GTGCTATTGCCCTTCTCTCATCATCATCTACTACTAGATGACAGGTGGCCCTTCGGGGAG 360

QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 Db 361 CTGCTCTGCAAGCTGGTGCACCTTCTGTCTATATCAACCTTTTACGGCAGCATCTGCTG 420
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 Db 421 CTGACCTGCATCTCTGTGCACAGTTCCTAGTGTGTGCCACCCACTGTGTCTGCTGCC 480
 QY 161 TyrArgThrArgArgHisAlaThrLeuGlyThrSerThrThrThrAlaLeuValLeu 180
 Db 481 TACCGGACCCGCGCAGCATGCTGGCTGGGCACCAACACCTGGGCTGGTGGTCTCTCCTC 540
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 Db 541 CAGCTGTGCTGCCACACTGGCTTCTCCACACGAGCTACATCAATGGCCAGATGATCTGG 600
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 Db 601 TATGACATGACCAAGAGAGAAATTTTATCGGCTTTTGGCTACGGCATAGTTCTGACA 660
 QY 221 LeuSerGlyPheLeuSerLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGlu 240
 Db 661 TTGCTGGCTTTT-TCCCTCCTTGGTCATTTTGGTGTCTTATTCATCTGATGGTCAGGAG 719
 QY 241 ProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValHis 260
 Db 720 CTTGATCAGCCAGGAGAGAACCTCATGAGACAGGCAACACACAGCCCGAGCGAGTCCAT 779
 QY 261 ProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrHis 280
 Db 780 CCGGACCATCTACTGTGTGGCTCTTCCACCTCTGTTTGTGGCTTCCATATCAC 839
 QY 281 SerLeuLeuLeuProHisHisLeuSerAlaPheSerGlyLeuProAlaLeuAspGly 300
 Db 840 TCGCTCTCTTACCTCACCATCTGCTTCTCTTCTCAGGACTGCCAGCTCTTGATGGC 899
 QY 301 SerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnPro 320
 Db 900 AGCCAGTGTGGCTTACAGATATGAGAGGCTCTCGTGTGTGAGAGTGTGAGAGCTCTCAACCC 959
 QY 321 SerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeu 339
 Db 960 AGTCTGTACTTCTTTCAGGGGGGCAAAATAGAGTACAGGCTCTCTCCAGAAACTG 1016
 RESULT 11
 ID ABQ79300 standard; DNA; 1020 BP.
 XX AC ABQ79300;
 XX DT 17-OCT-2002 (first entry)
 XX DE Human GPCR designated PFI-020' encoding sequence.
 XX KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
 XX KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
 XX KW disorder; PFI-020'; gene; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1020
 XX FT /*tag= a
 XX FT /product= "GPCR designated PFI-020"
 XX PN EP1215214-A1.
 XX PD 19-JUN-2002.
 XX PF 04-DEC-2001; 2001EP-00310137.
 XX PR 18-DEC-2000; 2000GB-00030855.
 XX PR 17-JAN-2001; 2001GB-00001222.

XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 XX Fidoack MD;
 XX
 XX WPI; 2002-510798/55.
 DR P-PSDB; ABB98146.
 XX
 XX New polynucleotide encoding G protein-coupled receptor PFI-020, useful
 PT e.g. for treating eating and sleeping disorders and for identifying
 PT specific modulators.
 XX
 XX Claim 1 (d); Page 12; 23pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a novel
 CC polypeptide belonging to the class of proteins known as G-protein coupled
 CC receptors (GPCRs). The activity of proteins of the invention may be
 CC described as, antidepressant and neuroleptic. Polynucleotides of the
 CC invention are used for recombinant expression of the G protein-coupled
 CC receptor (PFI-020) polypeptides, to create transgenic animals, as source
 CC of primers, probes, antisense sequences and ribozymes and in gene
 CC therapy. Therapeutic agents of the invention can be used to treat a wide
 CC range of disorders, particularly mood disorders, depression or arousal,
 CC especially eating and sleeping disorders. The current sequence represents
 CC a coding sequence for a human GPCR designated PFI-020.
 XX
 SQ Sequence 1020 BP; 200 A; 309 C; 252 G; 259 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,65e-162 Length: 1020
 Score: 1785.00 Matches: 337
 Percent Similarity: 99.12% Conservative: 1
 Best Local Similarity: 98.83% Mismatches: 1
 Query Match: 92.20% Indels: 2
 Gaps: 0

US-10-763-972-2 (1-360) x ABQ79300 (1-1020)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 Db 1 ATGCTGCCATTTTGTCTCTCCAGGGAAGCAGAGCGGGAGCGTCTGTGGAGCTCTG 60
 QY 21 LeuLeuGluGlyAlaSerArgMetGluLeuValAspMetAsnThrSerGlnGluGln 40
 Db 61 CTCTCTGAGGAGCCCTCCGGGACATGGAGAGGTGACATGAATACATCAGGAACAA 120
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 Db 121 GGTCTGTGCGAGTTCTCAGAGAGTACAGCAAGTCTACTCTCCCTGCGCTACAGTATC 180
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrPheSerTrpGlyGlnThr 80
 Db 181 ATCTTTATCTAGGGTGGCCACTAAATGGCACCTGTCTTGTGGCACCTCTGGGGCCAAACC 240
 QY 81 LysArgTrpSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuLeuTyr 100
 Db 241 AAGCGCTGGAGCTGTGCCACCACTATCTGTGAACCTGATGGTGGCCACCTGCTTTAT 300
 QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspArgTrpProPheGlyGlu 120
 Db 301 GTGCTATTGCCCTCTCATCATCACTACTACTAGTACAGAGTGGCCCTTCGGGGAG 360
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 Db 361 CTGCTCTGCAAGTGGTGGCACTTCTCTGTCTATCAACCTTTACGGCAGCATCTGCTG 420
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 Db 421 CTGACCTGCATCTCTGTCACCACTTCTAGGTGTGGCACCACCTGTTGCTGCTGCC 480
 QY 161 TyrArgThrArgArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180

Db 481 TACCGGACCGGACGATGCTGGTGGGACACGACACACCTGGGCGCTGGTGGTCTCCT 540
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleLeuGlyGlnMetIleTrp 200
 Db 541 CAGCTGTGCTGCCACACATGGGCTTCTCCACAGGACTACATCAATGCGCAGATGATCG 600
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 Db 601 TATGACATGACGACGCAAGAGATTTTGTATCGGCTTTTGTGCTACGGCATAGTCTTGACA 660
 QY 221 LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG 240
 Db 661 TTGTCTGGCTTCTTCTCCCTCTCTTGTGCTATTTGTGTGCTATTCACGATGGTCAAG 720
 QY 240 LuProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValH 260
 Db 721 AGCTGTATCAAGCAGAGGAGACCTCATGAGGACAGGACACAGCCGAGCCAGGTCC 780
 QY 260 isProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrH 280
 Db 781 ATCCGACCATCTCTACTGTGTGTGGCTCTTCCACCTCTGTGTGTGCTCTCCATATC 840
 QY 280 isSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG 300
 Db 841 ACTGCTCTTCTTCTACCTACCACTGCTTCTGCTTCTCAGGACTGCCAGCTCTTCTGATG 900
 QY 300 LysSerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnP 320
 Db 901 GCACCAAGTGTGGCTTCAAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCCTCAAC 960
 QY 320 roSerProValLeuSerPheLysGlyGlyLysAsnArgValArgCLeuLeuGlnLysLeu 339
 Db 961 CCAGTCTGTACTTCTTCTTCAAGGGGGGCAAAATAGAGTACAGCTCTCTCCAGAACTG 1019

RESULT 12
 AAD29667
 ID AAD29667 standard; cDNA; 1076 BP.
 XX
 AC AAD29667;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human G-protein coupled receptor (GCRC-1) cDNA.
 XX
 KW Human; G-protein coupled receptor; GCRC-1; cell proliferative disorder;
 KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
 KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
 KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
 KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic;
 KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
 KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
 KW neurotropic; neuroprotective; cardiant; immunosuppressive; anorectic;
 KW virucide; gene; ss.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 57..1076
 FT /*tag= a
 FT /product= "Human GCRC-1"
 XX
 PN WC02010387-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 25-JUL-2001; 2001WO-US023433.
 XX
 PR 27-JUL-2000; 2000US-0221478P.
 PR 03-AUG-2000; 2000US-0223268P.
 PR 21-AUG-2000; 2000US-0227054P.
 PR 08-SEP-2000; 2000US-0231121P.
 PR 13-SEP-2000; 2000US-0232243P.

PR 15-SEP-2000; 2000US-0232691P.
 PR 22-SEP-2000; 2000US-0235146P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
 PI Elliot VS, Ramkumar J, Baughn MR, Kailick DA, Walia NK, Hafalia AJA;
 PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC;
 PI Warren BA, Lee EA, Ding L;
 XX WPI; 2002-188744/24.
 DR P-PSDB; AAE18640.
 XX
 PT New human G-protein coupled receptor polypeptide for diagnosis,
 PT prevention and treatment of cell proliferative, neurological,
 PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
 PT disorders.
 XX
 PS Claim 5; Page 137-138; 150pp; English.
 XX
 CC The invention relates to novel human G-protein coupled receptors (GPCR)
 CC and their encoding polynucleotides. GPCR is useful as an immunogen for
 CC preparing monoclonal and polyclonal antibodies. GPCR is useful for
 CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
 CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
 CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
 CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
 CC cirrhosis, Crohn's disease), an autoimmune/inflammatory disorder (e.g.,
 CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,
 CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
 CC osteoporosis), and viral infections. GPCR is useful in a number of drug
 CC screening techniques, and to analyse the proteome of a tissue or cell
 CC type. GPCR is useful for creating knockin humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion, etc., among normal, carrier or affected individuals, and as
 CC hybridization probes for mapping naturally occurring genomic sequences.
 CC GPCR is useful in Southern or northern analysis, dot blot or other
 CC membrane-based technologies, in PCR technologies, in dipstick, pin,
 CC multiformat enzyme linked immunosorbent (ELISA)-like assays, and in
 CC microarrays utilising fluids or tissues from patients to detect altered
 CC GPCR expression. The present sequence is human GPCR-1 cDNA
 XX
 SQ Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.94e-162 Length: 1076
 Score: 1785.00 Matches: 337
 Percent Similarity: 99.12% Conservative: 1
 Best Local Similarity: 98.83% Mismatches: 1
 Query Match: 92.20% Indels: 2
 DB: 6 Gaps: 0
 US-10-763-972-2 (1-350) x RAD29667 (1-1076)
 QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20
 Db 57 ATGCTGTCATTTCCTTCCTCCAGGGGAAGCAGAGCGGGAGCGCTGTCGAGCTCTG 116
 QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLeuValAspMetAsnThrSerGlnGlu 40
 Db 117 CTCTTGAGGAGGACCTCCCGGACATGGAGAGGTGGACATGAATCATCATCAGGAACAA 176
 QY 41 GlyLeuCysGlnPheSerGluLysTyrLysGlnValTyrLeuSerLeuAlaTyrSerIle 60
 Db 177 GGTCTCTGCCAGTCTCAGAGAGTACACAGCAAGTCTACCTCTCCCTGCGCTACAGTATC 236
 QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuThrPheSerTrpGlyGlnThr 80
 Db 237 ATCTTTATCTAGGCTGCCACTAAATGGCACTGTCTTGTGGCACTCTCTGGGGGCCAAACC 296
 QY 81 LysArgTrpSerCysAlaThrThrTyrIleuValAsnLeuMetValAlaAspLeuLeuTyr 100
 Db 297 AAGCGCTGGAGCTGTGCCACACACCTATCTGTGTAACTGTGGTGGCGGACCTCTTTAT 356
 QY 101 ValLeuLeuProPheLeuIleIleThrTyrSerLeuAspAspArgTrpProPheGlyGlu 120
 Db 357 GTGCTATTGCCCTTCTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 416
 QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeu 140
 Db 417 CTGCTCTGCAAGCTGGTGCACCTTCTGTCTATATCAACCTTTACGGCAGCATCTCTGCTG 476
 QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160
 Db 477 CTGACCTGCATCTCTGTGCACCACTTCTAGGTGTGTGGACACCACTGTGTCTGCTGCC 536
 QY 161 TyrArgThrArgHisAlaTrpLeuGlyThrSerThrThrTrpAlaLeuValValLeu 180
 Db 537 TACCGGACCGCAGCATGCTGCTGGGCACCAACACCACTGGGCGCTGGTGGTCTCTC 596
 QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTrp 200
 Db 597 CAGCTGTGCCACACCTGCTTCTCCACACCGGACTACATCAATGGCCAGATGATCTGG 656
 QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220
 Db 657 TATGACATGACACGCAAGAGAAATTTGATCGGCTTTTGCCTACGGCATAGTCTTGACA 716
 QY 221 LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGln 240
 Db 717 TTGCTGCTGCTTCTTCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
 QY 240 LuProAspGlnAlaArgGlyGluProHisGluAspArgGlnHisSerProSerGlnValH 260
 Db 777 AGCTGTATCAAGCAGAGGAGAACTCATGAGGACAGGCAACACAGCCGCGGAGCTCC 836
 QY 260 isProAspHisProThrGlyValTrpProLeuHisProLeuPheCysAlaLeuProTyrH 280
 Db 837 ATCCGGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 QY 280 isSerLeuLeuProHisGlnLeuSerAlaPheSerGlyLeuProAlaLeuAspG 300
 Db 897 ACTGCTCTCTTCTACCTACCATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
 QY 300 LysSerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGlnLeuProGlnP 320
 Db 957 GCACCCAGTGTGGCTTACAGATATGAGGAGCTCTGCTGAGTGTGAGCAGCTGCTCAAC 1016
 QY 320 roSerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeu 339
 Db 1017 CCACTCTGCTACTTCTTCTTCAAGGGGGGCAAAATAGAGTCAAGCTCTCTCAGAAACTG 1075
 RESULT 13
 ID ADO30395 standard; cDNA; 1076 BP.
 XX ADO30395;
 AC ADO30395;
 DT 29-JUL-2004 (first entry)
 XX Human GPCR P2Y3L polynucleotide, SEQ ID NO:1498.
 DE
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytosstatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antiarrhoeic; antidiabetic;

virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 gene; ss.

Homo sapiens.

WO2004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

WPI; 2004-390329/36.

P-PSDB; ADO30394.

Novel mammalian G protein coupled receptors, useful for identifying
 compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 pectoris, Parkinson's disease.

Claim 15; SEQ ID NO 1498; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors
 (GPCRs) and nucleic acids encoding them. The invention also relates to
 sequences at least 90% identical to the GPCR proteins and nucleic acids
 of the invention; methods of treating, preventing or diagnosing diseases
 associated with GPCRs of the invention; methods of screening for
 compounds useful in the treatment of GPCR-related diseases; a transgenic
 mouse comprising a GPCR gene of the invention; a mouse comprising a
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 from the transgenic mice; kits comprising several mice, each of which has
 a mutation in a different GPCR gene of the invention; and kits comprising
 probes which hybridise to GPCR polynucleotides of the invention. The
 invention further discloses variants of the GPCR polypeptides and vectors
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 be used in the diagnosis, treatment or prevention of a wide variety of
 diseases including neurological disorders (e.g., Alzheimer's disease,
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 disorders of the adrenal gland; disorders of the colon or intestine
 (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 myocardial infarction); muscular disorders; blood disorders (e.g.,
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 diseases); and disorders of the kidney, liver, lung, breast, ovary,
 uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 nucleic acid of the invention. Note: the full sequence data for this
 patent did not form part of the printed specification; those sequences
 not shown were obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pat_sequences.

Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,94e-162 Length: 1076
 Score: 1785.00 Matches: 337
 Percent Similarity: 99.12% Conservative: 1
 Best Local Similarity: 98.83% Mismatches: 1
 Query Match: 92.20% Indels: 2
 12 Gaps: 0

US-10-763-972-2 (1-360) x ADO30395 (1-1076)

QY 1 MetLeuSerIleLeuLeuProSerArgGlySerArgSerGlySerArgGlyAlaLeu 20

DB 57 ATGCTGCTCATTTTCTTCCTTCAGGGGAAGAGAGAGCGGGAGCGCTGCGGAGCTCTG 116

QY 21 LeuLeuGluGlyAlaSerArgAspMetGluLysValAspMetAsnThrSerGlnGluGln 40

DB 117 CTCCTGGAGGGAGGCTCCCGGACATGAGAGGTGGACATGATACATACACAGAACAA 176

QY 41 GlyLeuCysGlnPheSerGluLysGlnValTyrLeuSerLeuAlaTyrSerIle 60

DB 177 GGTCTCTGCCAGTTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCTACAGTATC 236

QY 61 IlePheIleLeuGlyLeuProLeuAsnGlyThrValLeuTyrHisSerTyrGlnThr 80

DB 237 ATCTTTATCTAGGGCTGCCACTAAATGGCACTCTCTGTGGCACTCTCTGGGGCCAAAC 296

QY 81 LysArgTyrSerCysAlaThrThrTyrLeuValAsnLeuMetValAlaAspLeuTyr 100

DB 297 AAGCGCTGGAGCTGTGCCACCACCTATCTGTGTAACCTGATGGTGGCGGACCTCTTTAT 356

QY 101 ValLeuLeuProPheLeuIleThrTyrSerLeuAspAspArgTyrProPheGlyGlu 120

DB 357 GTGCTATTGGCCCTTCTCTCATCATCACCTACTCTAGTATGACAGTGGCCCTTCGGGAG 416

QY 121 LeuLeuCysLysLeuValHisPheLeuPheTyrIleAsnLeuTyrGlySerIleLeu 140

DB 417 CTGCTCTGCAAGCTGGTGCACTCTCTGTCTTATATCAACCTTTACGGCAGCATCTCTGTG 476

QY 141 LeuThrCysIleSerValHisGlnPheLeuGlyValCysHisProLeuCysSerLeuPro 160

DB 477 CTGACCTGCATCTCTGTGCACACAGTTCTCTAGGTGTGGCACCCACCTGTGTCTGCC 536

QY 161 TyrArgThrArgArgHisAlaTyrLeuGlyThrSerThrThrTyrAlaLeuValLeu 180

DB 537 TACCGACCCGAGGATGCTCTGCTGGGCACAGCACCACTTGGCCCTGGTGGTCTCTC 596

QY 181 GlnLeuLeuProThrLeuAlaPheSerHisThrAspTyrIleAsnGlyGlnMetIleTyr 200

DB 597 CAGTGTCTGCCACACTGGCTCTTCCACACAGGACTACATCAATGGCCAGATGATCTGG 656

QY 201 TyrAspMetThrSerGlnGluAsnPheAspArgLeuPheAlaTyrGlyIleValLeuThr 220

DB 657 TATGATCATACACAGCAAGAAATTTGATCGGCTTTTGGCTACGGCATAGTTCTGACA 716

QY 221 LeuSerGlyPheLeuSer--LeuLeuGlyHisPheGlyValLeuPheThrAspGlyGlnG 240

DB 717 TTGCTGGCTTTCTTCCCTCCCTCTGTCATTTTGGTGTGCTATTCTACTGATGCTCAGG 776

QY 240 LuProAspGlnAlaArgGlyClnProHisGluAspArgGlnHisSerProSerGlnValH 260

DB 777 AGCTGTATCAAGCCAGAGGAGAACCTCATGAGGACAGCAACACAGCCCGAGCGGTCC 836

QY 260 IsProAspHisProThrGlyValTyrProLeuHisProLeuPheCysAlaLeuProTyrH 280

DB 837 ATCCGACCATCTACTGTTGTGGCTCTTCCCTCTCTCTGTTTGTGGCTTCCATATC 896

QY 280 IsSerLeuLeuLeuProHisHisLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspG 300

DB 897 ACTCGCTCTTCTACTCCTCACCATCTGTTCTGCTTTCTCAGGACTGCCAGCTTTGATG 956

QY 300 LysSerGlnCysGlyLeuGlnAspMetGluAlaSerGlyGluCysGluGlnLeuProGlnP 320

DB 957 GCACCCAGTGTGGCTTACAGATATGGAGGCTCTGTGTAGTGTGAGCAGTGTGCTCTCAC 1016

QY 320 roSerProValLeuSerPheLysGlyLysAsnArgValArgLeuLeuGlnLysLeu 339

DB 1017 CCAGTCTCTGTACTTCTTCAAGGGGGGCAAAATAGAGTCAGGCTCTCTCCAGAACTG 1075

RESULT 14

AAS17747

ID AAS17747 standard; DNA; 850 BP.

XX AAS17747;
 AC 26-FEB-2002 (first entry)
 DT Human P2Y-like G protein-coupled receptor exon 1.
 DE
 XX Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;
 XX chronic obstructive pulmonary disease; nervous system disease;
 XX Parkinson's disease; multiple sclerosis; dementia; stroke;
 XX Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
 XX bacterial infection; fungal infection; protozoan infection;
 XX viral infection; pain; cancer; anorexia; bulimia; asthma; exon 1;
 XX acute heart failure; hypotension; hypertension; osteoporosis; diabetes;
 XX angina pectoris; myocardial infarction; ulcer; inflammation; allergy;
 XX psychotic disorder; neurological disorder; anxiety; schizophrenia;
 XX manic depression; delirium; severe mental retardation; dyskinesia.
 OS Homo sapiens.
 XX WO2001:85764-A2.
 XX 15-NOV-2001.
 XX 09-MAY-2001; 2001WO-EP005244.
 XX 11-MAY-2000; 2000US-0203582P.
 XX 21-FEB-2001; 2001US-0265857P.
 XX (FARB) BAYER AG.
 XX Ramakrishnan S;
 PI WPI; 2002-075242/10.
 DR
 XX
 PT New polynucleotides for producing P2Y-like G protein-coupled receptors
 PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-
 PT like GPCR, especially useful for treating pain, cancer or neurological
 PT disorders.
 XX
 XX Claim 1; Fig 4; 11app; English.
 PS
 CC The invention relates to an isolated polynucleotide encoding a P2Y-like G
 CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or
 CC allele, a host cell containing an expression vector comprising the
 CC polynucleotide and screening for agents that regulate the GPCR activity.
 CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide,
 CC which may be employed for screening agents that inhibit or regulate human
 CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is
 CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly
 CC COPD (chronic obstructive pulmonary disease), peripheral or central
 CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,
 CC dementia, stroke, Alzheimer's disease and many other diseases and
 CC disorders listed in the specification), benign prostatic hyperplasia or
 CC urinary incontinence. A pharmaceutical composition containing the
 CC modulators and/or regulators of P2Y-like GPCR is useful for modulating
 CC the activity of a P2Y-like GPCR. In particular, these are useful for
 CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,
 CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,
 CC acute heart failure, hypotension, hypertension, osteoporosis, diabetes,
 CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,
 CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic
 CC depression, delirium, severe mental retardation or dyskinesias). The
 CC present sequence is exon 1 of the P2Y-like GPCR of the invention
 XX
 SQ Sequence 850 BP; 165 A; 262 C; 201 G; 222 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9,46e-139 Length: 850
 Score: 1541.00 Matches: 283
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 79.60% Indels: 0

DB: 6 Gaps: 0
 US-10-763-972-2 (1-360) x AAS17747 (1-850)
 QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeuCysGlnPheSerGluLys 48
 DB 1 ATGGAGGAGGTGGACATGATACATCACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
 QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerLeilellePhelelleLeuGluValProLeu 68
 DB 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 120
 QY 69 AsnGlyThrValLeuTyrHisSerTyrGlyGlnThrLysArgTyrPsrCysAlaThrThr 88
 DB 121 AATGGCACTGTCTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACC 180
 QY 89 TyrLeuValAsnLeuMetValAlaAspLeuTyrValLeuLeuProPheLeuLeulle 108
 DB 181 TATCTGTGAACCTGATGGTGGCGAGCTGCTTTATGTGCTATTGCGCTTCTCATCATC 240
 QY 109 ThrTyrSerLeuAspAspArgTyrProPheGlyGluLeuLeuCysLysLeuValHisPhe 128
 DB 241 ACCTACTACTAGATGACAGGTGGCCCTTCGGGAGGTGCTCTGCAAGCTGGTGCATTC 300
 QY 129 LeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHisGln 148
 DB 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 360
 QY 149 PheLeuGlyValCysHisProLeuCysSerLeuProTyrArgThrArgGlnHisAlaTrp 168
 DB 361 TTCTAGGTGTGTCACCCCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 169 LeuGlyThrSerThrThrTyrAlaLeuValValLeuGlnLeuLeuProThrLeuAlaPhe 188
 DB 421 CTGGCACCAGCAGCACCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 189 SerHisThrAspTyrIleAsnGlyGlnMetIleTyrTrpAspMetThrSerGlnGluAsn 208
 DB 481 TCCACACGCGACTACATCAATGGCCAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 209 PheAspArgLeuPheAlaTyrGlyLeuValLeuThrLeuSerGlyPheLeuSerLeuLeu 228
 DB 541 TTTGATCGCTTTTGGCTACGGCATAGTTCGACATGTTCTGGCTTCTTCCCTCCTT 600
 QY 229 GlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgGlyGluPro 248
 DB 601 GGTCAATTTGGTGTGCTATTCTACCTGATGCTCAGGAGCTGATCAAGCCAGAGGAGAACCT 660
 QY 249 HisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyValTrp 268
 DB 661 CATGAGGACAGGCAACACAGCCCGAGCGAGTCCATCCGGACCATCTTACTGGTGTGG 720
 QY 269 ProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisHisLeu 288
 DB 721 CCTCTTCAACCTCTGTTTGTGGCTTCCATATCATCTGCTCTTCTACTCATCATCTG 780
 QY 289 LeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnAspMet 308
 DB 781 CTTTCTGTCTTCTCAGGACTCCAGCTCTTGTATGATGGCCAGCTGTGGCTTACAGATATG 840
 QY 309 GluAlaSer 311
 DB 841 GAGGCTCT 849
 RESULT 15
 ID ADO30397
 AC ADO30397;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Mouse GPCR P2Y3L polynucleotide, SEQ ID NO:1500.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytosolic; antinflammatory; vasotropic; antianigmal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW varicelle; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; gene; ss.
XX
OS Mus musculus.
XX
XX W02004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX
XX 09-SEP-2002; 2002US-0409303P.
XX
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
XX
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
FI
XX
XX WPI; 2004-390329/36.
DR P-PSDB; ADO30396.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 1500; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 906 BP; 173 A; 276 C; 216 G; 241 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.14e-92 Length: 906
Score: 1063.50 Matches: 207
Percent Similarity: 77.23% Conservative: 27
Best Local Similarity: 68.32% Mismatches: 66
Query Match: 54.93% Indels: 3
DB: 12 Gaps: 1

US-10-763-972-2 (1-360) x ADO30397 (1-906)
QY 29 MetGluLysValAspMetAsnThrSerGlnGluGlnGlyLeuCysGlnPheSerGluLys 48
Db 1 ATGGAGAGCTAGATATGAATGCTCTCAAGGGTCTGGCGCGCTGCCATCTTCAGAGAGC 60
QY 49 TyrLysGlnValTyrLeuSerLeuAlaTyrSerLeuLeuPheLeuLeuGlyLeuProLeu 68
Db 61 TACAGCAAGTCTACCTATCACTTAACCTACAGTCTCATCTTTATGCTAGGATGCCCTC 120
QY 69 AsnGlyThrValLeuTyrHisSerTyrGlyGlnThrLysArgTyrSerCysAlaThrThr 88
Db 121 AATGGGGCTGCTTATGGCTCTCTGGTGCCAAACCAAGCGCTGGAGCTGGCCACCATC 180
QY 99 TyrLeuValAsnLeuMetValAlaAspLeuLeuTyrValLeu---LeuProPheLeuLeu 107
Db 181 TACCTGATGAACCTGGTGGCTGACCTGCTTTATATGCTTAAGCTGCCCTTGTCTCATC 240
QY 108 IleThrTyrSerLeuAspAspArgTyrProPheGlyGluLeuLeuLeuValHis 127
Db 241 ATCACTACGGGTGGTGACACCTGGCTCTTTGGGAGATGCTGTGAGGTTGGTGGG 300
QY 128 PheLeuPheTyrIleAsnLeuTyrGlySerIleLeuLeuLeuThrCysIleSerValHis 147
Db 301 TTCCTGTTCTACACCAACCTCTACAGCAGCAGCTCTGCTGCTGAGCCTGCTCTCTACAC 360
QY 148 GlnPheLeuGlyValCysHisProLeuLeuCysSerLeuProTyrArgThrArgHisAla 167
Db 361 CGCTTCTTAGGAGTGTGCCACCTCTGAGCTCCTCTACCGGACTCACCGCAGCC 420
QY 168 TrpLeuGlyThrSerThrThrTrpAlaLeuValValLeuGlnLeuLeuProThrLeuAla 187
Db 421 TGGCAGGAGCTGTGCGCCACTGGACCTGGTAGTCTTCCAAATGCTGCCGACTGTGTC 480
QY 188 PheSerHisThrAspTyrIleAsnGlyGlnMetIleTrpTyrAspMetThrSerGlnGlu 207
Db 481 TTCTCCACACAGACTATGTAATGGCCAGGTGATCTGCTATGACACAGCCAGCCGAG 540
QY 208 AsnPheAspArgLeuPheAlaTyrGlyIleValLeuThrLeuSerGlyPhe--LeuSerL 227
Db 541 CAGTTTGATCATTTCTTCGCTTACAGCATAGTACTGACGTTATCTGGGTTGTCTTCCCC 600
QY 227 euLeuGlyHisPheGlyValLeuPheThrAspGlyGlnGluProAspGlnAlaArgGlyG 247
Db 601 TCTTTGATCATTTCTGGGTGCTACTCTCTGATGTTAGGAGCCTGACAAATCCAGTGAG 660
QY 247 luProHisGluAspArgGlnHisSerProSerGlnValHisProAspHisProThrGlyV 267
Db 661 GACCTCCCAACGACAGGCGCACACAGCGCTGCCAAGTCTATTCGAGCATCTCTCTGGTG 720
QY 267 alTrpProLeuHisProLeuPheCysAlaLeuProTyrHisSerLeuLeuLeuProHisH 287
Db 721 TGTGGCTTTTCACACTCTGTTTGTGGCTTCCACATGGCCCGCATCTTCTACTTGATC 780
QY 287 isLeuLeuSerAlaPheSerGlyLeuProAlaLeuAspGlySerGlnCysGlyLeuGlnA 307
Db 781 ATCCGCTTCTCCGAATGCACAGGACTGCCAGCTCTTTGTGGGAGCCAGCATGCCCTACAAG 840
QY 307 spMetGluAlaSerGlyGluCysGlnGlnLeuProGlnProSerProValLeuSerPheL 327
Db 841 GTCTGTAGGCTCTGGTAAAGCATGAGCAGCTGCCTCAATCCAGTCTCTTCTTGTCA 900

Qy 327 ysgly 328
Db 901 CAGGG 905

Search completed: November 10, 2004, 12:11:41
Job time : 602 secs

10/763972
Seq. IDs 1 & 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 08:36:32 ; Search time 4772 Seconds
(without alignments)
10722.434 Million cell updates/sec

Title: US-10-763-972-1

Perfect score: 1082
Sequence: 1 atgctgtccattttgttcc.....ccagggttgacacatctgg 1082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_br.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1082	100.0	1082	6	BD187416
2	1082	100.0	1082	6	AX458306
3	1082	100.0	1145	9	HS345013
4	1082	100.0	1334	6	AX646427
5	1082	100.0	1334	9	AB085670
6	1082	100.0	3143	6	AX385511
7	1082	100.0	154502	2	AC026960
8	1082	100.0	167084	9	AC092999
9	1071	99.0	163958	2	AC021773
10	1059	97.9	1108	6	AX921825
11	1007	93.1	1019	9	AF411108
12	1002.8	92.7	1020	6	BD187417
13	1002.8	92.7	1020	6	AX458308
14	1002.8	92.7	1076	6	AX375230
15	996.4	92.1	1002	6	BD095704
16	850	78.6	850	6	AX385514
17	779.4	72.0	1140	6	CQ734310
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22	510	47.1	510	6	AX147768
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24	396.4	36.6	681	6	AX244718
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26	235.8	21.8	1163	5	GD2Y33
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28	227.8	21.1	2025	6	AX270919
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30	227.8	21.1	2025	9	HSU07225
31	226.2	20.9	2257	9	BC028135
32	224.6	20.8	1134	9	AX136753
33	224.6	20.8	1974	6	CQ720945
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37	222	20.5	551	6	AX230145
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42	202.2	18.7	2138	10	MUSP2UREC
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ALIGNMENTS

RESULT 1	BD187416	1082 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD187416				
DEFINITION	Novel polypeptide.				
ACCESSION	BD187416				
VERSION	BD187416.1 GI:32997155				
KEYWORDS	JP 2003009885-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1082)				
AUTHORS	Fidock,M.D.				
TITLE	Novel polypeptide				
JOURNAL	Patent: JP 2003009885-A 1 14-JAN-2003;				
COMMENT	Pfizer Ltd (BP (GB) only), Pfizer Inc (US JP EP except GB)				
	OS homo sapiens				
	PN JP 2003009885-A/1				
	PD 14-JAN-2003				
	PF 17-DEC-2001 JP 2001382707				
	PR 18-DEC-2000 GB 0030855.1,17-JAN-2001 GB 0101222.8 PI				
	mark david fidock				
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Best Local Similarity	100.0%;	Pred. No. 6.7e-267;
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DB 121 GGTCTCTGCCAGTCTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCTACAGTATC 180
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DEFINITION Sequence 1 from Patent EP1215214.
ACCESSION AX458306
VERSION AX458306.1 GI:21725001
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fidoock, M.D.
TITLE Novel polypeptide
JOURNAL Patent; EP 1215214-A 1 19-JUN-2002;
Pfizer Limited (GB); PFIZER INC. (US)
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source location/Qualifiers
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Query Match 100.0%; Score 1082; DB 6; Length 1082;
Best Local Similarity 100.0%; Pred. No. 6.7e-267;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS HSA345013 Homo sapiens P2Y2-like gene for nucleoside/nucleotide receptor.
DEFINITION
ACCESSION AJ345013
VERSION AJ345013.1 GI:34495183
KEYWORDS nucleoside/nucleotide receptor; P2Y2-like gene.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Bruss, M., Bonisch, H. and Kugelgen, I.
TITLE Molecular identification and functional characterization of a new G protein-coupled nucleoside-/nucleotide receptor
JOURNAL Unpublished
2 (bases 1 to 1145)
AUTHORS Bruess, M.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Bruess M., Pharmacology and Toxicology, University of Bonn, Reuterstrasse 2 b, D-53113, GERMANY

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gene
CDS

ORIGIN

Query Match 100.0%; Score 1082; DB 9; Length 1145;
Best Local Similarity 100.0%; Pred. No. 6.7e-267;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 ATGCTGTCCATTTGCTTCTTCCAGGGAGAGCAGAGCGGAGCCCTCGTGGAGCTCTG 69
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JOURNAL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-Ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081)

COMMENT This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].

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Query Match 100.0%; Score 1082; DB 9; Length 1334;
Best Local Similarity 100.0%; Pred. No. 6.8e-267; Indels 0; Gaps 0;
Matches 1082; Conservative 0; Mismatches 0;

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DB 117 ATGCTGTCCTATTTGCTTCCAGGGGAAGCAGAGCGGAGCGCTCTGGAGCTCTG 176
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DB 237 GGTCTCTGCCAGTCTTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCTACAGTATC 296
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DB 1197 GG 1198

RESULT 6
LOCUS AX365511 3143 bp DNA linear PAT 21-FEB-2002
DEFINITION Sequence 1 from Patent WO0185764.
ACCESSION AX365511
VERSION AX365511.1 GI:18873666
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ramakrishnan, S.
TITLE Regulation of human p2y-like g protein-coupled receptor
JOURNAL Patent; WO 0185764-A 1 15-NOV-2001;
Bayer Aktiengesellschaft (DE)
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ORIGIN
Query Match 100.0%; Score 1082; DB 6; Length 3143;
Best Local Similarity 100.0%; Pred. No. 7.3e-267; Indels 0; Gaps 0;
Matches 1082; Conservative 0; Mismatches 0;

QY 1 ATGCTGTCCATTTTCTTCTTCTCAGGGGAGCAGAGCGGAGCCGCTGCTGAGCTCTG 60
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 1 (bases 1 to 164502)
 Homo sapiens chromosome 3, clone RP11-170K4
 Unpublished
 2 (bases 1 to 164502)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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 Direct Submission
 Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 13, 2000 this sequence version replaced gi:17328839.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
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 Center project name: L8491
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 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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          Zimmer,A. and Zody,M.
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          Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
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          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
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          Center code: WIBR
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          Contact: sequence.submissions@genome.wi.mit.edu
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          * This record will be updated with the finished sequence
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Best Local Similarity 99.9%; Pred. No. 6 8e-264; Mismatches 0; Indels 1; Gaps 1;
Matches 1082; Conservative 0

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QY 121 GGTCTCTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGCCCTACAGTATC 180
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DB 98463 CTGCTCTGAGCTGTGGCACTTCTGTTCTATCAACCTTTACGGCAGCATCTGCTG 98522

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LOCUS Sequence 165 from Patent WO02068649.
DEFINITION AX921825
ACCESSION AX921825
VERSION AX921825.1 GI:40215364
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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PATENT: WO 02068649-A 165 06-SEP-2002;
Curagen Corporation (US)
Location/Qualifiers

ORIGIN

Query Match 97.9%; Score 1059; DB 6; Length 1108;
Best Local Similarity 99.8%; Pred. No. 5.5e-261;
Matches 1081; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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 ACCESSION AF411108.1 GI:16566321
 VERSION AF411108.1
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O.,
 Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
 TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
 JOURNAL Gene 275 (1), 83-91 (2001)
 MEDLINE 21458557
 PUBMED 11574155
 REFERENCE 2 (bases 1 to 1019)
 AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O.,
 Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
 Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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BD187417
LOCUS BD187417 1020 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel polypeptide.
ACCESSION BD187417
VERSION BD187417.1 GI:32997156
KEYWORDS JP 2003009885-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS Fidoock, M.D.
TITLE Novel polypeptide
JOURNAL Patent: JP 2003009885-A 2 14-JAN-2003;
Pfizer Ltd (EP/GB only), Pfizer Inc (US JP BP except GB)
COMMENT OS Homo sapiens
PN JP 2003009885-A/2
PD 14-JAN-2003
PF 17-DEC-2001 JP 2001382707
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mark david fidoock
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BD187417
LOCUS BD187417 1020 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel polypeptide.
ACCESSION BD187417
VERSION BD187417.1 GI:32997156
KEYWORDS JP 2003009885-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS Fidoock, M.D.
TITLE Novel polypeptide
JOURNAL Patent: JP 2003009885-A 2 14-JAN-2003;
Pfizer Ltd (EP/GB only), Pfizer Inc (US JP BP except GB)
COMMENT OS Homo sapiens
PN JP 2003009885-A/2
PD 14-JAN-2003
PF 17-DEC-2001 JP 2001382707
PR 18-DEC-2000 GB 0030855.1, 17-JAN-2001 GB 0101222.8 PI
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QY 1 ATGCTGCCAATTTTGGCTTCCAGGGGAAGCAGAGGCGGAGCGTGGTGGAGCTCTG 60
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RESULT 13
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LOCUS AX458308 1020 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 3 from Patent EP1215214.
ACCESSION AX458308
VERSION AX458308.1 GI:21725002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fidoock, M.D.
TITLE Novel polypeptide
JOURNAL Patent: EP 1215214-A 3 19-JUN-2002;
Pfizer Limited (GB); PFIZER INC. (US)
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Query Match          92.7%; Score 1002.8; DB 6; Length 1020;
Best Local Similarity 99.6%; Pred. No. 1.5e-246;
Matches 1016; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
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 DEFINITION Sequence 20 from Patent W00210387.
 ACCESSION AX375230
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 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS
 Thornton, M., Patterson, C., Lal, P., Burford, N., Yue, H., Gandhi, A.R.,
 Elliot, V.S., Ramkumar, J., Baughn, M.R., Kallik, D.A., Walla, N.K.,
 Hall, A.J., Yao, M.G., Lu, Y., Tribouley, C.M., Policky, J.L.,
 Kearney, B., Gaudi, R.C., Warren, B.A. and Ding, L.
 G-protein coupled receptors
 Patent: WO 0210387-A 20 07-FEB-2002;
 Incyte Genomics, Inc. (US)
 TITLE
 JOURNAL
 FEATURES Location/Qualifiers

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ORIGIN

Query Match 92.7%; Score 1002.8; DB 6; Length 1076;
 Best Local Similarity 99.6%; Pred. No. 1.5e-246;
 Matches 1016; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

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 Db 57 ATGCTGTCCATTTTGTCTTCCAGGGGAAGCAGAGCGGAGCCGCTGCGAGCTCTG 116
 QY 61 CTCTTGGAGGAGCTTCCGGGACATGGAGAGGTGACATGAATATACACAGAAACA 120
 Db 117 CTCTTGGAGGAGCTTCCGGGACATGGAGAGGTGACATGAATATACACAGAAACA 176
 QY 121 GGTCTCTGCCAGTCTCAGAGAGGTACAGCAAGTCTACCTCTCCCTGGGCTACAGTATC 180
 Db 177 GGTCTCTGCCAGTCTCAGAGAGGTACAGCAAGTCTACCTCTCCCTGGGCTACAGTATC 236
 QY 181 ATCTTTATCTAGGCTGCCACTAAATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACC 240
 Db 237 ATCTTTATCTAGGCTGCCACTAAATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACC 296
 QY 241 AAGCGTGGAGCTGTGCCACCACTATCTGCTGAACCTGATGTGGCGGACCTGCTTTAT 300
 Db 297 AAGCGTGGAGCTGTGCCACCACTATCTGCTGAACCTGATGTGGCGGACCTGCTTTAT 356
 QY 301 GTGCTATTGCGCTTCTCTCATCATCACTACTCTAGATGACAGTGGCCCTTCGGGGAG 360
 Db 357 GTGCTATTGCGCTTCTCTCATCATCACTACTCTAGATGACAGTGGCCCTTCGGGGAG 416
 QY 361 CTGCTCTGCAAGCTGTGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCTGCTG 420
 Db 417 CTGCTCTGCAAGCTGTGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCTGCTG 476
 QY 421 CTGACCTGCTCTGTGCAACAGTCTCTAGTGTGCAACCACTGCTGCTGCTGCTGCTG 480
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 QY 481 TACCGGACCCGACGATGCTGTGCTGGGCAACAGCAACCTGGGCGCTGTGGTCTCTC 540
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 QY 541 CAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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 Db 657 TATGACATGACAGCAAGAGATTTTGTGCGCTTTTGTGCTACGCACTAGTCTTGACA 716
 QY 661 TTGCTGCTCTTCTTTT - CCTCTCTGCTCATTTTGTGCTTATCTAGTGGTCAAG 718
 Db 717 TTGCTGCTCTTCTTTTCTTCTCTGCTCATTTTGTGCTTATCTAGTGGTCAAG 776
 QY 719 AGCTGTATCAGCAGAGGAGAACTCATGAGGACGACGACGACGACGACGACGACGACG 778
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 QY 779 ATCCGAGACCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 838
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 QY 899 GCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958

Db	957	GCACCCAGTGTGGCCTACAAGATATGAGGCGCTCTGGTGTAGTGTGACGACTGCCTCAAC	1018
Qy	959	CCAGTCTCTACTTTTCTTTTCAAGGGGGGCAAAAATAGAGTCAGGCTCTCCAGAAACTGA	1018
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LOCUS			linear
DEFINITION			Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.
ACCESSION			BD095704
VERSION			BD095704.1
KEYWORDS			GI:22641292
SOURCE			WO 0148188-A/16.
ORGANISM			Homo sapiens (human)
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1002)
TITLE			Matsumoto,S., Oda,T., Saito,Y., Noriyuki, Morikawa, Yoshida,K., Suwa,M., Sugiyama,T., Kishimoto,T., Kanzaki,K., Yasuda,S. and Inoue,Y.
JOURNAL			Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use Patent: WO 0148188-A 16 05-JUL-2001.
COMMENT			HELIX RESEARCH INSTITUTE,SHUNICHIRO MATSUMOTO,TAKAKI ODA,YOKO SAITO, NORIYUKI MORIKAWA,KENJI YOSHIDA,MAKIKO SUWA,TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO SUGIYAMA, YOSHIHISA INOUE OS Homo sapiens (human) PN WO 0148188-A/16 PD 05-JUL-2001 PF 28-DEC-2000 WO 2000JP009408 PR 28-DEC-1999 JP 99P 375152,31-MAR-2000 JP OOP 101339 PI SHUNICHIRO MATSUMOTO,TAKAKI ODA,YOKO SAITO,NORIYUKI PI MORIKAWA,KENJI YOSHIDA, MAKIKO SUWA,TOMOYASU SUGIYAMA,TOSHIMITSU KISHIMOTO,KOJI KANZAKI, SHINICHIRO SUGIYAMA, YOSHIHISA INOUE PI SHINICHIRO YASUDA, YOSHIHISA INOUE PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C07K14/705, PC C07K16/28, PC C12P21/02,C12Q1/02,C12Q1/68,A61K31/711,A61K48/00,A61P43/00, PC G01N33/15, PC G01N33/50 CC Novel guanosine triphosphate-bound protein-coupled receptors CC encoding them, and their production and use CC encoding them, and their production and use FH Key Location/Qualifiers FT source 1..1002 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..1002 /organism='Homo sapiens' /mol_type='Genomic DNA' /db_xref='taxon:9606'
FEATURES			source
ORIGIN			
			Query Match 92.1%; Score 996.4; DB 6; Length 1002; Best Local Similarity 99.9%; Pred. No. 6.6e-245; Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	85	ATGAGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCGAGTTCTCAGAGAAG	144
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Qy	145	TACAGCAAGTCTACCTCTGCGCTACAGTATCATCTTTATCTCCTAGGGCTGCCACTA	204
Db	61	TACAGCAAGTCTACCTCTGCGCTACAGTATCATCTTTATCTCCTAGGGCTGCCACTA	120
Qy	205	AATGGCACTGCTTTGTGGCACTCTCTGGGGGGCAAAACCAAGCCCTGGAGCTGTGCCACCAC	264
Db	121	AATGGCACTGCTTTGTGGCACTCTCTGGGGGGCAAAACCAAGCCCTGGAGCTGTGCCACCAC	180

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 09:14:47 ; Search time 611 Seconds
(without alignments)

9534.556 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:

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- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1082	100.0	1334	15	US-10-017-161-707
4	1082	100.0	1334	15	US-10-292-798-619
5	1082	100.0	3143	15	US-10-275-910-1
6	1059	97.9	1108	16	US-10-072-012-165
7	1006	93.0	1017	10	US-09-885-453-3
8	1006	93.0	1017	15	US-10-079-384-5
9	1002.8	92.7	1020	15	US-10-023-586B-3
10	1002.8	92.7	1020	17	US-10-763-972-3
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12	996.4	92.1	1002	15	US-10-088-726-25

13	851	78.7	851	15	US-10-275-910-6
14	850	78.6	850	15	US-10-275-910-4
15	510	47.1	510	10	US-09-782-974C-13
c 16	396.4	36.6	681	11	US-09-801-944B-47
17	370	34.2	585	11	US-09-801-944B-56
18	227.8	21.1	2025	15	US-10-225-567A-216
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26	178.6	16.5	1429	16	US-10-305-720-1068
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33	163.2	15.1	1832	15	US-10-225-567A-222
34	163.2	15.1	1832	15	US-10-172-118-994
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ALIGNMENTS

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US-10-023-586B-1
; Sequence 1, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US20030166882A1el Polypeptide
; FILE REFERENCE: PC10960AGPR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-586B-1

Query Match 100.0%; Score 1082; DB 15; Length 1082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCTGTCCATTTTGTCTTCCTCCAGGGGAGCAGAGCGGCGCTGAGCTCTG 60

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; Sequence 1, Application US/10763972
; Publication NO. US20040137500A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; APPLICANT: Pfizer Inc.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10960B
; CURRENT APPLICATION NUMBER: US/10/763,972
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-763-972-1
Query Match 100.0%; Score 1082; DB 17; Length 1082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTCCATTTTGTCTTCTTCCAGGGGAAGCAGAGCGGAGCCGTGTTGGAGCTCTG 60
DB 1 ATGCTGTCCATTTTGTCTTCTTCCAGGGGAAGCAGAGCGGAGCCGTGTTGGAGCTCTG 60
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RESULT 3
US-10-017-161-707
; Sequence 707, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 707
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1334)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(715)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(1134)
US-10-017-161-707
Query Match 100.0%; Score 1082; DB 15; Length 1334;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGTCCATTTTGTCTTCTTCAGGGGAAGCAGAGCGGGAGCCGTGTGGAGCTCTG 60

US-1

Matches 1082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATGCTGTCCATTTTGCTTCTCCTCAGGGGAAGCAGAAAGCGGAGCCGCTCGTGAGCTCTG	60
Db	436	ATGCTGTCCATTTTGCTTCTTCCAGGGGAAGCAGAAAGCGGAGCCGCTCGTGAGCTCTG	495
Qy	61	CTCCTGGAGGAGCCTCCGGGACATGGAGAGGTGGACATGAATAATACACAGGAACAA	120
Db	496	CTCCTGGAGGAGCCTCCGGGACATGGAGAGGTGGACATGAATAATACACAGGAACAA	555
Qy	121	GGTCTCTGCCAGTTCTCAGAGAGAGTCAAGCAAGTCTACCTCTCCCTGGGCTACAGTATC	180
Db	556	GGTCTCTGCCAGTTCTCAGAGAGAGTCAAGCAAGTCTACCTCTCCCTGGGCTACAGTATC	615
Qy	181	ATCTTTATCTAGGGTCGCCATAATGGCACTGCTCTGTGTGGCACTCTCTGGGGCCAAACC	240
Db	616	ATCTTTATCTAGGGTCGCCATAATGGCACTCTCTGTGTGGCACTCTCTGGGGCCAAACC	675
Qy	241	AAGCGCTGGAGCTGTGCCACACACTACTCTGGTGAACCTGATGTGGGCGGACCTGCTTTAT	300
Db	676	AAGCGCTGGAGCTGTGCCACACACTACTCTGGTGAACCTGATGTGGGCGGACCTGCTTTAT	735
Qy	301	GTGCTATTGGCCTTCCTCATCATCACCTACTCATAGATGACAGGTGGCCCTTCGGGGAG	360
Db	736	GTGCTATTGGCCTTCCTCATCATCACCTACTCATAGATGACAGGTGGCCCTTCGGGGAG	795
Qy	361	CTGCTCTGAAGCTGGTGCACTTCTCTTATATCAACCTTTACGGCAGCATCCTGCTG	420
Db	796	CTGCTCTGAAGCTGGTGCACTTCTCTTATATCAACCTTTACGGCAGCATCCTGCTG	855
Qy	421	CTGACCTGCACTCTCTGTGCCACCACTTCTAGGTGTGTGCCACCCACCTGTGTCTGCC	480
Db	856	CTGACCTGCACTCTCTGTGCCACCACTTCTAGGTGTGTGCCACCCACCTGTGTCTGCC	915
Qy	481	TACGGGACCGCAGGCAATGCTGTGGGACCAAGCACCACTTGGGCGCTGGTGGTCTC	540
Db	916	TACGGGACCGCAGGCAATGCTGTGGGACCAAGCACCACTTGGGCGCTGGTGGTCTC	975
Qy	541	CAGCTGCTGCCACACTGGCCCTTCTCCACACGGACTACATCAATGGCCAGATCATCTG	600
Db	976	CAGCTGCTGCCACACTGGCCCTTCTCCACACGGACTACATCAATGGCCAGATCATCTG	1035
Qy	601	TATGACATGACCAAGCAAGAAATTTTGATCGGCTTTTGCCCTACGGCATAGTTCCTGACA	660
Db	1036	TATGACATGACCAAGCAAGAAATTTTGATCGGCTTTTGCCCTACGGCATAGTTCCTGACA	1095
Qy	661	TTGTCCTGGCTTCTTTCCCTCTCTGGTCAATTTTGGTGTGCTATTCTACTGATGTGCAGAG	720
Db	1096	TTGTCCTGGCTTCTTTCCCTCTCTGGTCAATTTTGGTGTGCTATTCTACTGATGTGCAGAG	1155
Qy	721	CCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTCCAT	780
Db	1156	CCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTCCAT	1215
Qy	781	CCGGACCATCCTACTGTGTGTGGCTTCTCACCTCTGTTTGTGGCTTCCATATCAC	840
Db	1216	CCGGACCATCCTACTGTGTGTGGCTTCTCACCTCTGTTTGTGGCTTCCATATCAC	1275
Qy	841	TCGCTCTCTTACCTCCACATCTGCTTTTCTGCTTTTCTCAGGACTGCCAGCTCTTGATGGC	900
Db	1276	TCGCTCTCTTACCTCCACATCTGCTTTTCTGCTTTTCTCAGGACTGCCAGCTCTTGATGGC	1335
Qy	901	AGCCAGTGTGGCTTACAAGATATGGAGGCCTCTGGTGAGTGTGACAGCTGCCTCAACC	960
Db	1336	AGCCAGTGTGGCTTACAAGATATGGAGGCCTCTGGTGAGTGTGACAGCTGCCTCAACC	1395
Qy	961	AGTCTCTGTACTTTCTTTCAAGGGGGGCAAAAATAGATCAGGCTCCTCCAGAACTGAGG	1020
Db	1396	AGTCTCTGTACTTTCTTTCAAGGGGGGCAAAAATAGATCAGGCTCCTCCAGAACTGAGG	1455
Qy	1021	CAGAACAGTTGGGTGAGATCCAGCTGGGAGGAGAGATGCCACAGGGTGTGAACAGATCT	1080
Db	1456	CAGAACAGTTGGGTGAGATCCAGCTGGGAGGAGAGATGCCACAGGGTGTGAACAGATCT	1515

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Db      12  ATGCTGTCCATTTCCTTCCTCCAGGGGAGCAGAGCGGAGCCGCTCGTGAGCTCTG 71
Qy      61  CTCCTGAGGAGGAGCTCCCGGACATGGAGAGTGGACATGAATACATCACAGGAACAA 120
Db      72  CTCCTGAGGAGGAGCTCCCGGACATGGAGAGTGGACATGAATACATCACAGGAACAA 131
Qy     121  GGTCTCTGCCAGTTCTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
Db     132  GGTCTCTGCCAGTTCTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 191
Qy     181  ATCTTTATCTAGGCTGCCACTTAAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACC 240
Db     192  ATCTTTATCTAGGCTGCCACTTAAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACC 251
Qy     241  AAGCGCTGGAGCTGTGCCACCACTTCTGTGAACCTGTATGTGGCGGACCTGCTTTAT 300
Db     252  AAGCGCTGGAGCTGTGCCACCACTTCTGTGAACCTGTATGTGGCGGACCTGCTTTAT 311
Qy     301  GTGCTATGGCTTCCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 360
Db     312  GTGCTATGGCTTCCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 371
Qy     361  CTGCTCTGCAAGCTGGTGCACTTCTCTGTATCAACCTTTACGGCAGCATCTGCTG 420
Db     372  CTGCTCTGCAAGCTGGTGCACTTCTCTGTATCAACCTTTACGGCAGCATCTGCTG 431
Qy     421  CTGACCTGTGCATCTGTGTGCACCACTTCTAGGTGTGTGCCACCACTGTGTCGTCGCC 480
Db     432  CTGACCTGTGCATCTGTGTGCACCACTTCTAGGTGTGTGCCACCACTGTGTCGTCGCC 491
Qy     481  TACCGGACCCGACGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
Db     492  TACCGGACCCGACGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 551
Qy     541  CAGCTGTGTGCCACACCTGTGTGCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
Db     552  CAGCTGTGTGCCACACCTGTGTGCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 611
Qy     601  TATGACATGACCAAGAGATTTTGTGCGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGC 660
Db     612  TATGACATGACCAAGAGATTTTGTGCGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGC 671
Qy     661  TTGTCTGCTTTCTTTCCCTCCTTGTGTCATTTTGGTGTGTCATTTCACTGATGTCAGGAG 720
Db     672  TTGTCTGCTTTCTTTCCCTCCTTGTGTCATTTTGGTGTGTCATTTCACTGATGTCAGGAG 730
Qy     721  CCTGATCAAGCCAGGAGAACCTCATGAGGACAGGCAACAGCCCGAGCCAGGTCCTCAT 780
Db     731  CCTGATCAAGCCAGGAGAACCTCATGAGGACAGGCAACAGCCCGAGCCAGGTCCTCAT 790
Qy     781  CCGGACCATCTACTGTGTGTGCGCTTTTCAACCTCTGTTTGTGCGCTTTTGTGCGCTTT 840
Db     791  CCGGACCATCTACTGTGTGTGCGCTTTTCAACCTCTGTTTGTGCGCTTTTGTGCGCTTT 850
Qy     841  TCGCTCCTTTTACCTCAACATCTGCTTTTCTGCTTTTCTGAGGATGCGAGCTCTTGTAGGC 900
Db     851  TCGCTCCTTTTACCTCAACATCTGCTTTTCTGCTTTTCTGAGGATGCGAGCTCTTGTAGGC 910
Qy     901  AG-CCAGTGTGGCTTACAAGATATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
Db     911  AGCCAGTGTGGCTTACAAGATATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970
Qy     960  CAGTCTGTACTTTTCAAGGGGGGCAAAATAGAGTCAAGTCAAGTCTCTCAGAAACTGAG 1019
Db     971  CAGTCTGTACTTTTCAAGGGGGGCAAAATAGAGTCAAGTCAAGTCTCTCAGAAACTGAG 1030
Qy    1020  GCAGAACAGTGTGGTGAAGATCCAGCTGGGAGGAGATGCGCAGGTTGAACAGATC 1079
Db    1031  GCAGAACAGTGTGGTGAAGATCCAGCTGGGAGGAGATGCGCAGGTTGAACAGATC 1090
Qy    1080  TGG 1082
Db    1091  TGG 1093

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RESULT 7
US-09-885-453-3
; Sequence 3, Application US/09885453
; Publication No. US2003008080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRxi10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA sequence
; LOCATION: (1)..(1017)
; OTHER INFORMATION: GPCRxi6 DNA sequence
US-09-885-453-3

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Query Match      93.0%; Score 1006; DB 10; Length 1017;
Best Local Similarity 99.9%; Pred. No. 2.8e-303;
Matches 1017; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy      1  ATGCTGTCCATTTCCTTCCTCCAGGGGAGCAGAGCGGAGCCGCTCGTGAGCTCTG 60
Db      1  ATGCTGTCCATTTCCTTCCTCCAGGGGAGCAGAGCGGAGCCGCTCGTGAGCTCTG 60
Qy     61  CTCCTGAGGAGGAGCTCCCGGACATGGAGAGTGGACATGAATACATCACAGGAACAA 120
Db     61  CTCCTGAGGAGGAGCTCCCGGACATGGAGAGTGGACATGAATACATCACAGGAACAA 120
Qy    121  GGTCTCTGCCAGTTCCTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
Db    121  GGTCTCTGCCAGTTCCTCAGAGAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATC 180
Qy    181  ATCTTTATCTTAGGCTGCCACTTAAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACC 240
Db    181  ATCTTTATCTTAGGCTGCCACTTAAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACC 240
Qy    241  AAGCGCTGGAGCTGTGCCACCACTTCTGCTGTAACCTGTGTCGTCGTCGTCCTTTAT 300
Db    241  AAGCGCTGGAGCTGTGCCACCACTTCTGCTGTAACCTGTGTCGTCGTCGTCCTTTAT 300
Qy    301  GTGCTATTGCCCTTCTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 360
Db    301  GTGCTATTGCCCTTCTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAG 360
Qy    361  CTGCTCTCAAGCTGTGTGCATCTTCTGTCTTATATCAACCTTTACGGCAGCATCTGCTG 420
Db    361  CTGCTCTCAAGCTGTGTGCATCTTCTGTCTTATATCAACCTTTACGGCAGCATCTGCTG 420
Qy    421  CTGACCTGCATCTCTGTGCACCACTTCTAGGTGTGTGCCACCACTGTGTCTGCTGCC 480
Db    421  CTGACCTGCATCTCTGTGCACCACTTCTAGGTGTGTGCCACCACTGTGTCTGCTGCC 480
Qy    481  TACCGGACCCGACGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
Db    481  TACCGGACCCGACGATGCTGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
Qy    541  CAGCTGTGTGCCACACCTGCTTCTCCACACGAGCTACATCAATGCGCAGATCATCTGG 600
Db    541  CAGCTGTGTGCCACACCTGCTTCTCCACACGAGCTACATCAATGCGCAGATCATCTGG 600
Qy    601  TATGACATGACCAAGAGATTTTGTGCGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGC 660
Db    601  TATGACATGACCAAGAGATTTTGTGCGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGC 660

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; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-586B-3

Query Match          92.7%; Score 1002.8; DB 15; Length 1020;
Best Local Similarity 99.6%; Pred. No. 2.8e-302;
Matches 1016; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 ATGCTGCTCCATTTGCTTCCCTTCCAGGGGAAGCAGAGCGGAGCGCGTGGAGCTCTG 60
DB 1 ATGCTGCTCCATTTGCTTCCCTTCCAGGGGAAGCAGAGCGGAGCGCGTGGAGCTCTG 60

QY 61 CTCCTGGAGGAGCCTCCCGGACATGGAAGGTGGACATGATACATACAGAGACAA 120
DB 61 CTCCTGGAGGAGCCTCCCGGACATGGAAGGTGGACATGATACATACAGAGACAA 120

QY 121 GGTCTCTGCGAGTTCTCAGAGAAGTACAAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATC 180
DB 121 GGTCTCTGCGAGTTCTCAGAGAAGTACAAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATC 180

QY 181 ATCTTTATCTAGGGCTGCACCTAAATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACC 240
DB 181 ATCTTTATCTAGGGCTGCACCTAAATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACC 240

QY 241 AAGCGCTGGAGCTGTGCCACACCTATCTGGTGAACCTGATGGTGGCGACCTGCTTTAT 300
DB 241 AAGCGCTGGAGCTGTGCCACACCTATCTGGTGAACCTGATGGTGGCGACCTGCTTTAT 300

QY 301 GTGCTATTCGCTTCTCTCATCATCACCTACTCTAGATGACAGGTGGCCCTTCGGGGAG 360
DB 301 GTGCTATTCGCTTCTCTCATCATCACCTACTCTAGATGACAGGTGGCCCTTCGGGGAG 360

QY 361 CTGCTCTGCAAGCTGGTGCACTTCTCTTATATCAACTTTACGGCAGCATCTCTGCTG 420
DB 361 CTGCTCTGCAAGCTGGTGCACTTCTCTTATATCAACTTTACGGCAGCATCTCTGCTG 420

QY 421 CTGACCTTGCATCTCTGTGCAACCAAGTCTCTAGGTGTGTGGCCACCACTGTGTGCTGCC 480
DB 421 CTGACCTTGCATCTCTGTGCAACCAAGTCTCTAGGTGTGTGGCCACCACTGTGTGCTGCC 480

QY 481 TACCGGACCCGAGCATGCTGGCTGGGACACAGCACCTGGGCGCTGGTGGTCTC 540
DB 481 TACCGGACCCGAGCATGCTGGCTGGGACACAGCACCTGGGCGCTGGTGGTCTC 540

QY 541 CAGCTGTCTGCCACACTGGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGG 600
DB 541 CAGCTGTCTGCCACACTGGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGG 600

QY 601 TATGATGACAGCAGCAGAGAAATTTGATCGGCTTTTGGCTACGGGATAGTCTGACA 660
DB 601 TATGATGACAGCAGCAGAGAAATTTGATCGGCTTTTGGCTACGGGATAGTCTGACA 660

QY 661 TTGCTGGCTTTCTTTTCCCTCTCTGCTCAATTTGGTGTGCTATTCACATGAGTTCAGG 718
DB 661 TTGCTGGCTTTCTTTTCCCTCTCTGCTCAATTTGGTGTGCTATTCACATGAGTTCAGG 718

QY 719 AGCCTGATCAAGCCAGAGAGAACTCATAGGACAGGCAACACAGCCCGAGCCAGGTCC 778
DB 719 AGCCTGATCAAGCCAGAGAGAACTCATAGGACAGGCAACACAGCCCGAGCCAGGTCC 778

QY 779 ATCCGGACCATCTACTGGTGTGGGCTCTTCACTCTCTGTTTGGCTTCCCTCATATC 838
DB 779 ATCCGGACCATCTACTGGTGTGGGCTCTTCACTCTCTGTTTGGCTTCCCTCATATC 838

QY 839 ACTCGCTCCTTCTACTCACCATCTGCTTTCTGCTTTCTAGGACTGCCAGCTCTTGATG 898
DB 839 ACTCGCTCCTTCTACTCACCATCTGCTTTCTGCTTTCTAGGACTGCCAGCTCTTGATG 898

QY 899 GCAGCCAGTGTGGCTACAGATATGAGAGGCTCTGCTGAGTGTGACAGCTGGCTCAAC 958
DB 899 GCAGCCAGTGTGGCTACAGATATGAGAGGCTCTGCTGAGTGTGACAGCTGGCTCAAC 958

QY 901 GCACCCAGTGTGGCTTACAAGATATGAGAGGCTCTGCTGAGTGTGAGCAGCTGCCTCAAC 960
DB 901 GCACCCAGTGTGGCTTACAAGATATGAGAGGCTCTGCTGAGTGTGAGCAGCTGCCTCAAC 960

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541	Db	 CAGCTGTCGCCACACTGGCCCTTCTCCACACGGACTCATCAATGCGCAGATGATCTGG	600
601	Qy	TATGACATGACACAGCAAGAGAAATTTTGATCGGCTTTTGGCTTACGGCATAGTTCTGACA	660
601	Db	TATGACATGACACAGCAAGAGAAATTTTGATCGGCTTTTGGCTTACGGCATAGTTCTGACA	660
661	Qy	TTGTCGTGGCTTTCTTT--CCCTCCTTGGTCATTTTGGTGTGCTATTCACTGATGTCAGG	718
661	Db	TTGTCGTGGCTTTCTTTTCCCCCTCTTGGTCATTTTGGTGTGCTATTCACTGATGTCAGG	720
719	Qy	AGCCTGATCAAGCCAGAGAGAACTCATGAGACAGGCAACACAGCCGAGCCAGGTC	778
721	Db	AGCCTGATCAAGCCAGAGAGAACTCATGAGACAGGCAACACAGCCGAGCCAGGTC	780
779	Qy	ATCGGACCATCTACTGTTGTGTGGCCCTTTCACCCCTCTGTTTGTGCCCCCTCCATATC	838
781	Db	ATCGGACCATCTACTGTTGTGTGGCCCTTTCACCCCTCTGTTTGTGCCCCCTCCATATC	840
839	Qy	ACTCGTCCTTCTACCTCACCATCTGCTTCTGCTTCTCAGGACACTGCCAGCTCTTGATG	898
841	Db	ACTCGTCCTTCTACCTCACCATCTGCTTCTGCTTCTCAGGACACTGCCAGCTCTTGATG	900
899	Qy	GCAGCCAGTGTGGCTACAAGATATGAGGCGCTCTGGTGAGTGTGAGCAGCTGCCTCAAC	958
901	Db	GCACCCAGTGTGGCTACAGATATGAGGCGCTCTGGTGAGTGTGAGCAGCTGCCTCAAC	960
959	Qy	CCAGTCCTGACTTTCTTTTCAAGGGGGGCAAAATAGAGTCAGGCTCTCCAGAAACTGA	1018
961	Db	CCAGTCCTGACTTTCTTTTCAAGGGGGGCAAAATAGAGTCAGGCTCTCCAGAAACTGA	1020

RESULT 11

361	QY	CTGCTCTGCAAGCTGGTGCACTTCCGTGTTCTATATCAACCTTTAGCGACGACTCTGCTG	420
417	Db	CTGCTCTGCAAGCTGGTGCACTTCCGTGTTCTATATCAACCTTTAGCGACGACTCTGCTG	476
421	QY	CTGACCTGCATCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCCACTGTGTTCTGCTGCC	480
477	Db	CTGACCTGCATCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCCACTGTGTTCTGCTGCC	536
481	QY	TACCGGACCCGAGGATGCTGGCTGGGACACAGACACCACTGGGCGCTGTGTTCTGCTC	540
537	Db	TACCGGACCCGAGGATGCTGGCTGGGACACAGACACCACTGGGCGCTGTGTTCTGCTC	596
541	QY	CAGCTGTGTCGCCACACATCGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGG	600
597	Db	CAGCTGTGTCGCCACACATCGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGG	656
601	QY	TATGACATGACCAAGCAAGATTTTGATCGGCTTTTGGCTACGGCATAGTCTTGACA	660
657	Db	TATGACATGACCAAGCAAGATTTTGATCGGCTTTTGGCTACGGCATAGTCTTGACA	716
661	QY	TTGCTGTGCTTTTCTTTTCCCTCTGTTGGTCAATTTTGGTGTGCTATTCACTGATGTTGAGG	718
717	Db	TTGCTGTGCTTTTCTTTTCCCTCTGTTGGTCAATTTTGGTGTGCTATTCACTGATGTTGAGG	776
719	QY	AGCTGTATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTCC	778
777	Db	AGCTGTATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTCC	836
779	QY	ATCCGGACCATCTTACTGTTGGCTCTTCAACCTCTGTTTGTGCTTGTGCTTCCATATC	838
837	Db	ATCCGGACCATCTTACTGTTGGCTCTTCAACCTCTGTTTGTGCTTGTGCTTCCATATC	896
839	QY	ACTGCTCCTTTCTACCTCAACATCTGCTTTCTGCTTTCTGAGACTGCCAGCTCTTGATG	898
897	Db	ACTGCTCCTTTCTACCTCAACATCTGCTTTCTGCTTTCTGAGACTGCCAGCTCTTGATG	956
899	QY	GCAGCCAGTGTGGCTACAGATATGAGGCTCTCTGTTGATGTGAGCAGCTGCCCTCAAC	958
957	Db	GCAGCCAGTGTGGCTACAGATATGAGGCTCTCTGTTGATGTGAGCAGCTGCCCTCAAC	1016

QY 959 CCAGTCTGTACTTTCTTCAAGGGGGCAAAATAGAGTCAGGCTCCTCCAGAACTGA 1018
 DB 1017 CCAGTCTGTACTTTCTTCAAGGGGGCAAAATAGAGTCAGGCTCCTCCAGAACTGA 1076

RESULT 12
 US-10-088-726-25
 ; Sequence 25, Application US/10088726
 ; Publication No. US20030157558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsumoto et al.
 ; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND
 ; TITLE OF INVENTION: THEREOF, AND PRODUCTION AND USES THEREOF
 ; FILE REFERENCE: 62514
 ; CURRENT APPLICATION NUMBER: US/10/088,726
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 25
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-088-726-25

Query Match 92.1%; Score 996.4; DB 15; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 2.7e-300;
 Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 85 ATGGAGAGGTGGACATGATATACATACAGAAACAAAGGTCTCTGCCAGTTCTCAGAGAAG 144
 DB 1 ATGGAGAGGTGGACATGATATACATACAGAAACAAAGGTCTCTGCCAGTTCTCAGAGAAG 60

QY 145 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGTGCACATA 204
 DB 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGTGCACATA 120

QY 205 AATGGCACTGCTGTGGCACTCTCTGGGCAACCAAGCGCTGGAGCTGCGCACACC 264
 DB 121 AATGGCACTGCTGTGGCACTCTCTGGGCAACCAAGCGCTGGAGCTGCGCACACC 180

QY 265 TATCTGTGAACCTGATGCTGGCGACCTGCTTTATGTGCTATGCTCTTCTCATCATC 324
 DB 181 TATCTGTGAACCTGATGCTGGCGACCTGCTTTATGTGCTATGCTCTTCTCATCATC 240

QY 325 ACCTACTCAGTATGATGAGTGGCGCTTGGGAGCTGCTGCAAGTGTGCACTTC 384
 DB 241 ACCTACTCAGTATGATGAGTGGCGCTTGGGAGCTGCTGCAAGTGTGCACTTC 300

QY 385 CTGCTTTATATCAACCTTTACGCGACATCTCTGCTGACCTGATCTCTGTCACACAG 444
 DB 301 CTGCTTTATATCAACCTTTACGCGACATCTCTGCTGACCTGATCTCTGTCACACAG 360

QY 445 TTCTAGGTGTGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
 DB 361 TTCTAGGTGTGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 505 CTGGGCAACGACCACTGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
 DB 421 CTGGGCAACGACCACTGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 565 TCCCAACGAGCTACATCAATGCGCAGATGATCTGATGATGATGATGATGATGATGATGATG 624
 DB 481 TCCCAACGAGCTACATCAATGCGCAGATGATCTGATGATGATGATGATGATGATGATGATG 540

QY 625 TTTGATCGGCTTTTCTGCTACGCGATGTTCTGACATTTGCTGGCTTTCTTCCCTCCTT 684

DB 541 TTTGATCGGCTTTTCTGCTACGGCATAGTTCTGACATTTGTGGCTTTCTTTCCCTCCTT 600
 QY 685 GGTCAATTTTGTGTGCTATTACTGATGCTCAGGAGCTGATCAAGCCAGGAGAACCT 744
 DB 601 GGTCAATTTTGTGTGCTATTACTGATGCTCAGGAGCTGATCAAGCCAGGAGAACCT 660

QY 745 CATGAGGACAGGCAACACAGCCCGAGGCTCCATCCGAGCCATCTCTACTGCTGTGG 804
 DB 661 CATGAGGACAGGCAACACAGCCCGAGGCTCCATCCGAGCCATCTCTACTGCTGTGG 720

QY 805 CCTCTTCACTCTGCTTTTGTGCTCCCTCCATATACATGCTGCTCTTCTACCTCAACATCTG 864
 DB 721 CCTCTTCACTCTGCTTTTGTGCTCCCTCCATATACATGCTGCTCTTCTACCTCAACATCTG 780

QY 865 CTCTCTGCTTTCTCAGGACTGCCAGCTCTTCTGATGGCAGCCAGTGTGGCTTACAAGATATG 924
 DB 781 CTCTCTGCTTTCTCAGGACTGCCAGCTCTTCTGATGGCAGCCAGTGTGGCTTACAAGATATG 840

QY 925 GAGGCTCTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGCTTCTTTCAAGGG 984
 DB 841 GAGGCTCTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGCTTCTTTCAAGGG 900

QY 985 GGCATAATAGAGTCAGGCTCTCTCAGAACTGAGGAGCAAGTGTGGTGCATCCA 1044
 DB 901 GGCATAATAGAGTCAGGCTCTCTCAGAACTGAGGAGCAAGTGTGGTGCATCCA 960

QY 1045 GCTGGGAGAGAGATGCCAGGGTTGAACAGATCTCG 1082
 DB 961 GCTGGGAGAGAGATGCCAGGGTTGAACAGATCTCG 998

RESULT 13
 US-10-275-910-6
 ; Sequence 6, Application US/10275910
 ; Publication No. US20030166142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 4974.00885
 ; CURRENT APPLICATION NUMBER: US/10/275,910
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: US 60/203,582
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: US 60/269,857
 ; PRIOR FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 851
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-275-910-6

Query Match 78.7%; Score 851; DB 15; Length 851;
 Best Local Similarity 100.0%; Pred. No. 6.7e-255;
 Matches 851; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 ATGGAGAGGTGGACATGATATACATACAGAAACAAAGGTCTCTGCCAGTTCTCAGAGAAG 144
 DB 1 ATGGAGAGGTGGACATGATATACATACAGAAACAAAGGTCTCTGCCAGTTCTCAGAGAAG 60

QY 145 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGTGCACATA 204
 DB 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGTGCACATA 120

QY 205 AATGGCACTGCTGTGGCACTCTCTGGGCAACCAAGCGCTGGAGCTGCGCACACC 264
 DB 121 AATGGCACTGCTGTGGCACTCTCTGGGCAACCAAGCGCTGGAGCTGCGCACACC 180

QY 265 TATCTGTGAACCTGATGCTGGGCGCTGCTTTATGTGCTATGCTCTTCTCATCATC 324
 DB 181 TATCTGTGAACCTGATGCTGGGCGCTGCTTTATGTGCTATGCTCTTCTCATCATC 240

QY	325	ACCTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGTGTGCACATTC	384
DB	241	ACCTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGTGTGCACATTC	300
QY	385	CTGTTCTATATCAACCTTTTACGGCAGCATCCTCTGCTGACCTGCATCTCTGTGCACCAAG	444
DB	301	CTGTTCTATATCAACCTTTTACGGCAGCATCCTCTGCTGACCTGCATCTCTGTGCACCAAG	360
QY	445	TTCTTAGTGTGTGCCACCCACTGTGTTCTGCTGCCCTACCGGACCCGCGAGGCATGCTCGG	504
DB	361	TTCTTAGTGTGTGCCACCCACTGTGTTCTGCTGCCCTACCGGACCCGCGAGGCATGCTCGG	420
QY	505	CTGGCACCAGCACCACCTGCGGCGCTGGTGTCTCCAGCTGCTGCCACACTGGCCTTC	564
DB	421	CTGGGCAACAGCACACCTGGGCGCTGGTGTCTCCAGCTGCTGCCACACTGGCCTTC	480
QY	565	TCCACACGGGACTACATCAATGGCCAGATGATCTGTGTATGACATGACCCAGCCAGAGAAAT	624
DB	481	TCCACACGGGACTACATCAATGGCCAGATGATCTGTGTATGACATGACCCAGCCAGAGAAAT	540
QY	625	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGTCTGGCTTTCTTTCCCTCCTT	684
DB	541	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGTCTGGCTTTCTTTCCCTCCTT	600
QY	685	GGTCATTTTGGTGTCTATTCTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT	744
DB	601	GGTCATTTTGGTGTCTATTCTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT	660
QY	745	CATGAGGACAGGCAACACAGCCGAGCAGTGTCATCCGACCATCTCTACTGTGTGTGG	804
DB	661	CATGAGGACAGGCAACACAGCCGAGCAGTGTCATCCGACCATCTCTACTGTGTGTGG	720
QY	805	CCTCTTCACCCTCTGTTTGTGGCTTCCATATCACTCGCTTCTTACCTCACCATCTG	864
DB	721	CCTCTTCACCCTCTGTTTGTGGCTTCCATATCACTCGCTTCTTACCTCACCATCTG	780
QY	865	CTTCTGCTTTTCTCAGGACTGCCAGCTTTGATCGGACCGAGTGTGGCTTACAAGATATG	924
DB	781	CTTCTGCTTTTCTCAGGACTGCCAGCTTTGATCGGACCGAGTGTGGCTTACAAGATATG	840
QY	925	GAGGCGCTCTGG	935
DB	841	GAGGCGCTCTGG	851
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US-10-275-910-4			
; Sequence 4, Application US/10275910			
; Publication No. US20030166142A1			
; GENERAL INFORMATION:			
; APPLICANT: Ramakrishnan, Shyam			
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR			
; FILE REFERENCE: 4974.00885			
; CURRENT APPLICATION NUMBER: US/10/275,910			
; CURRENT FILING DATE: 2002-11-12			
; PRIOR APPLICATION NUMBER: US 60/203,582			
; PRIOR FILING DATE: 2000-05-11			
; PRIOR APPLICATION NUMBER: US 60/269,857			
; PRIOR FILING DATE: 2001-02-21			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 850			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-275-910-4			
Query Match 78.6%; Score 850; DB 15; Length 850;			
Best Local Similarity 100.0%; Pred. No. 1.4e-254;			
Matches 850; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	85	ATGCGAGAAGGTGGCATGTAATCATCAGGAAACAAGTCTCTGCCAGTTCCTAGAGAAG	1444

Db	1	ATGGAGAAGGTGGACATGAATACATCACAGGAACAAGGTCTCTGCCAGTTCTCTCAGAGAAG	60
QY	145	TACAAGCAAGTGTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA	204
Db	61	TACAAGCAAGTGTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA	120
QY	205	AATGGCACTGTCTTGTGGCACTCCTCGGGCCAAACAAAGCGCTGGAGCTGTGCCACCAACC	264
Db	121	AATGGCACTGTCTTGTGGCACTCCTCGGGCCAAACAAAGCGCTGGAGCTGTGCCACCAACC	180
QY	265	TATCTGGTGAACCTGATAGTGTGGCCGACCTGTCTTTATGTGTCTATTTGCCCTTCTTCATCATC	324
Db	181	TATCTGGTGAACCTGATAGTGTGGCCGACCTGTCTTTATGTGTCTATTTGCCCTTCTTCATCATC	240
QY	325	ACCTACTCCTACATGACACAGGTGGCCCTTCGGGGAGCTGCTGTGCAAGCTGGTGCACCTTC	384
Db	241	ACCTACTCCTACATGACACAGGTGGCCCTTCGGGGAGCTGCTGTGCAAGCTGGTGCACCTTC	300
QY	385	CTGTCTTATATCAACCTTTACCGCAGCATCTCTGCTGTGACCTGTGCAATCTCTGTGCACCAAG	444
Db	301	CTGTCTTATATCAACCTTTACCGCAGCATCTCTGCTGTGACCTGTGCAATCTCTGTGCACCAAG	360
QY	445	TTCTTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTACCGGACCCGCGAGGCATGCTCTGG	504
Db	361	TTCTTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTACCGGACCCGCGAGGCATGCTCTGG	420
QY	505	CTGGCACCAAGCACCACCTGGGCGCTGGTGGTCTCTCCAGCTGTGCTGCCACACATGGCCCTTC	564
Db	421	CTGGCACCAAGCACCACCTGGGCGCTGGTGGTCTCTCCAGCTGTGCTGCCACACATGGCCCTTC	480
QY	565	TCCACACAGCACTACATCAATAGCCAGATGATCTGGTATGACATGACATGACCCAGAGAAAT	624
Db	481	TCCACACAGCACTACATCAATAGCCAGATGATCTGGTATGACATGACATGACCCAGAGAAAT	540
QY	625	TTTGTATCGGCTTTTGTGCTACGCAATAGTTCTGCATTTGTGGCTTTCTTTCCCTCCCTT	684
Db	541	TTTGTATCGGCTTTTGTGCTACGCAATAGTTCTGCATTTGTGGCTTTCTTTCCCTCCCTT	600
QY	685	GGTCATTTTGGTGTGCTATTCACTGATGTGTGAGAGCCTGATCAAGCCAGAGAGAACCT	744
Db	601	GGTCATTTTGGTGTGCTATTCACTGATGTGTGAGAGCCTGATCAAGCCAGAGAGAACCT	660
QY	745	CATGAGACAGGCAACACAGCCGAGCCAGTCCATCCGGACCACTCTACTGTGTGTGG	804
Db	661	CATGAGACAGGCAACACAGCCGAGCCAGTCCATCCGGACCACTCTACTGTGTGTGG	720
QY	805	CCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCACCATCTG	864
Db	721	CCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCACCATCTG	780
QY	865	CTTCTCTCTTCTCAGACACTGCGAGCTCTTGATGGAGCCAGTGTGGCTTACAGAGATG	924
Db	781	CTTCTCTCTTCTCAGACACTGCGAGCTCTTGATGGAGCCAGTGTGGCTTACAGAGATG	840
QY	925	GAGGCTCTGTG	934
Db	841	GAGGCTCTGTG	850

RESULT 15
 US-09-782-974C-13
 ; Sequence 13, Application US/09782974C
 ; Publication No. US20030082534A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogeli, Gabriel
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Wood, Linda S.
 ; APPLICANT: Parodi, Luis A.
 ; FILE OF INVENTION: No. US20030082534A1
 ; TITLE REFERENCE: 41USPHRM311
 ; CURRENT APPLICATION NUMBER: US/09/782, 974C
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIORITY APPLICATION NUMBER: 60/165, 838

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RESULT 15
US-09-782-974C-13
; Sequence 13, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1a1 (
; FILE REFERENCE: 41USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838

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3 Protein Coupled Receptor

; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/199,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-13

Query Match 47.1%; Score 510; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-148;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	307	TTGCCCTTCCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTC	366
Db	61	TTGCCCTTCCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTC	120
Qy	367	TGCAGCTGTGACATTCCTGTTCTATATCAACCTTTACGGGAGATCCTGCTGTGACC	426
Db	121	TGCAAGCTGTGACATTCCTGTTCTATATCAACCTTTACGGGAGATCCTGCTGTGACC	180
Qy	427	TGATCTCTGTGCACCACTTCCTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTACCGG	486
Db	181	TGATCTCTGTGCACCACTTCCTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTACCGG	240
Qy	487	ACCGCAGGATGCTGGCTGGGACACAGCACCACTGGGCCCTGTGTGTCCTCCAGCTG	546
Db	241	ACCGCAGGATGCTGGCTGGGACACAGCACCACTGGGCCCTGTGTGTCCTCCAGCTG	300
Qy	547	CTGCCACACTGGCTTCTCCACAGGACTACATCAATGGCCAGATGATCTGGTATGAC	606
Db	301	CTGCCACACTGGCTTCTCCACAGGACTACATCAATGGCCAGATGATCTGGTATGAC	360
Qy	607	ATGACCAAGCAAGAGATTTTGATCGGCTTTTTCCTACGGCATAGTCTTGACATTTGCT	666
Db	361	ATGACCAAGCAAGAGATTTTGATCGGCTTTTTCCTACGGCATAGTCTTGACATTTGCT	420
Qy	667	GGCTTTCTTTCCTCCTGCTGCTATTTTGGTGTGCTATTCACTGATGGTCAGGACCTGAT	726
Db	421	GGCTTTCTTTCCTCCTGCTGCTATTTTGGTGTGCTATTCACTGATGGTCAGGACCTGAT	480
Qy	727	CAAGCCAGAGGAGAACCTCATAGGACAGG	756
Db	481	CAAGCCAGAGGAGAACCTCATAGGACAGG	510

Search completed: November 10, 2004, 12:01:33
Job time : 613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 08:44:17 ; Search time 114 Seconds
(without alignments)
6746.259 Million cell updates/sec

Title: US-10-763-972-1
Perfect score: 1082
Sequence: 1 atgctgtccattttgtctcc.....ccagggttgacacagatctgg 1082

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227.8	21.1	2025	4	US-09-016-434-1482
2	227.8	21.1	2025	4	US-09-814-915A-74
3	203.8	18.8	1842	1	US-08-442-134A-1
4	203.8	18.8	1842	1	US-08-444-581B-1
5	203.8	18.8	1842	1	US-08-446-088A-1
6	178.6	16.5	1429	4	US-08-016-434-1068
7	178.6	16.5	1429	4	US-08-077-173D-1
8	164.8	15.2	984	3	US-08-513-974B-57
9	164.8	15.2	984	4	US-09-461-436B-57
10	164.8	15.2	1023	3	US-08-513-974B-379
11	163.2	15.1	1571	4	US-09-016-434-1108
12	156.8	14.5	984	3	US-08-459-046-1
13	156.8	14.5	984	4	US-08-102-710B-1
14	148.8	13.8	984	3	US-08-513-974B-41
15	148.8	13.8	984	4	US-09-461-436B-41
16	148.8	13.8	1020	3	US-08-513-974B-370
17	97.4	9.0	1773	4	US-09-016-434-1405
18	95.8	8.9	998	4	US-08-432-174A-3
19	95.6	8.8	1892	4	US-09-900-699A-1
20	92	8.5	1475	1	US-08-097-938-1
21	92	8.5	1475	1	US-08-476-000-1
22	92	8.5	1475	1	US-08-472-840-1
23	92	8.5	1475	2	US-08-476-976-1
24	92	8.5	1475	3	US-08-474-410-1
25	92	8.5	1475	3	US-08-486-673B-1
26	92	8.5	2732	1	US-08-476-000-60
27	92	8.5	2732	1	US-08-472-840-60

28	92	8.5	2732	2	US-08-476-976-60
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30	92	8.5	2732	3	US-08-486-673B-60
31	91.4	8.4	1205	1	US-08-417-103-13
32	91.4	8.4	1634	1	US-07-816-283-1
33	91.4	8.4	1634	1	US-08-417-103-1
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35	89.8	8.3	3055	4	US-09-016-434-1456
36	88.4	8.2	1020	4	US-09-170-496D-31
37	88.4	8.2	1020	4	US-09-170-496D-181
38	88.4	8.2	1900	1	US-09-016-434-1484
39	88.4	8.2	1901	1	US-08-153-848-43
40	88.4	8.2	1901	3	US-09-299-843A-43
41	88.4	8.2	1901	3	US-09-088-337B-43
42	88.4	8.2	1901	5	PCT-US93-11153-43
43	88.4	8.2	2453	5	PCT-US95-07180-1
44	87.4	8.1	1119	4	US-09-170-496D-65
45	87.4	8.1	1119	4	US-09-170-496D-199

ALIGNMENTS

RESULT 1
US-09-016-434-1482
; Sequence 1482, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2025 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G984506
; US-09-016-434-1482

Query Match 21.1%; Score 227.8; DB 4; Length 2025;
Best Local Similarity 56.4%; Pred. No. 6.8e-53;


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Db      1155 GTGCTACTACTGCTGGTGG 1175
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RESULT 3
US-08-442-134A-1
; Sequence 1, Application US/08442134A
; Patent No. 5596088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seitzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-442-134A-1

Query Match      18.8%; Score 203.8; DB 1; Length 1842;
Best Local Similarity 56.3%; Pred.No.2.7e-46;
Matches 485; Conservative 0; Mismatches 362; Indels 14; Gaps 5;

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Qy      187 ATCTTAGGGTGCACCTAAATGGCACTGTCTTGTGGCACTCTCTGGGCGCAACCAAGCGC 246
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Db      249 TGGAAATGGTCCACACATATATGTTCACCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 308
Qy      307 T---TGCCCTTCCTCATCATCACCTACTCATAGATCACAGGTGGCCCTTCGGGGAGGTG 363

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-444-581B-1

Query Match 18.8%; Score 203.8; DB 1; Length 1842;
Best Local Similarity 56.3%; Pred. No. 2.7e-46;
Matches 485; Conservative 0; Mismatches 362; Indels 14; Gaps 5;
QY 127 TGCAGATCTCAGAGAGTCAACAGAGTCACTCTCCCTGGCTACATATATATATTT 186
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DB 189 GTGCTTGGCTGTCTGACGCGCTGGGCTCTACATCTCTGTGGCGGCTCAAGACC 248
QY 247 TGGAGCTGTGCCACCATCTATCTGGTGAACCTGATGTGGCGGACCTGCTTTATGCTA 306
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QY 364 CTCTGCAAGCTGTGACCTCTCTGCTTCTATATCAACCTTTACGGCAGCATCTCTGCTG 423
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QY 424 ACCTGCACTCTGTGACCACTCTCTAGTGTGTGCCACCACTGTGTGCTGCGCTAC 483
DB 429 ACCTGCACTCTGTGACCACTCTCTAGTGTGTGCCACCACTGTGTGCTGCGCTAC 488
QY 484 CGGACCCGCGAGGATGTGCTGGCGGACCAACCACTGTGGGCGCTGTGCTGCCAG 543
DB 489 GGCGCGCGCGCTACGCTGCGCGGCTGGCGGGCGCTGTGGG---TGTGTGTGCGGC 545
QY 544 CTGCTGCGGCACTGGGCTTCTCCCAACGAGCTATCAATGCGGAGATGATCTGGTAT 603
DB 546 TGGCAGGCGCGGCTCTCTATTGTCCACCAAGCGCGGCGGCTTAACCTGCCAC 605
QY 604 GACATGACCAAGAGATTTGTGCGCTTTTGGCTTTCCTACGCACTGTCTGACATTG 663
DB 606 GACACCTGGGACCCGAGCTCTTACGCGCTTGTGGCGCTTACAGCTCAGTCTGCGGC 665
QY 664 TCTGGCTT---TCTTTCCTCTTGGTCAATTTGGTGTGCTTATCACTGATGCTCAGGAGC 721
DB 666 CTGCTCTTGGCGGTGCGCTTGGCGTCTATCTTGTCTGTACGTGTCTGCTGCGGCA 725
QY 722 CTGATCAAGCAGGAGACCTCATGAGGACAGGCAACACAGCCCGGAGCCAGTCCATC 781

DB 726 CTGTAAAGCCAGCCTACGGGACCTCGGGCGGCGCTAGGGCCAGGCAAGTCCGTG 785
QY 782 CGGACCATCTACTGTTGTGGCTCTTACCTCTCTGTTTGTGCGCTTCCATATCACT 841
DB 786 CGACCATCGCGGTGTGCTGCTCTTCCGCTCTCTTCCCTGCGCAATCCAGTCAAC 845
QY 842 CGCTCTCTTACTCCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTTGTATGSCA 901
DB 846 CGCACCCTCTACTACTCTCTCCGCT---CGCTGGACCTCAGTCCACACCTCAAGGCC 902
QY 902 GCAGTGTGGCTCAAGATATGAGGCTCTGTGAGTGTGAGCAGTGTCTCAACCCA 961
DB 903 ATCAACATGGCTCAAGGT---TACCCGGTGGCGAGTGTAAACAGTTCCTTGAOCCC 959
QY 962 GTCCTGTACTTCTTTCAAGG 982
DB 960 GTGCTTACTTCTGCTGGTGGG 980

RESULT 5

US-08-446-088A-1
Sequence 1, Application US/08446088A
Patent No. 5691156

GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.

TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691156th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1842 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 57..1181

US-08-446-088A-1

Query Match 18.8%; Score 203.8; DB 1; Length 1842;
Best Local Similarity 56.3%; Pred. No. 2.7e-46;

	Matches	485;	Conservative	0;	Mismatches	362;	Indels	14;	Gaps	57;
Qy	127	TGCCAGTCTCAGAGAAAGTCAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTT	186							
Db	129	TGCCGCTTCAACGAGAGACTTCAAGTACGTGTGCTGCTGTGTCTACGGGTGGTGTGC	188							
Qy	187	ATCCTAGGGTGCCACTTAATAGGCACCTGTCTGTGGACACTCTCTGGGGCCAAACCAAGGC	245							
Db	189	GTGCTTGGGCTGTGTGAACGGCGTGGGCTCTACATCTTCTTGTGGCGCTCAAGACC	248							
Qy	247	TGGAGCTGTGCAACCACTATCTGGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCTA	306							
Db	249	TGGAATCGTCCACACATATATGTCCACCTGGCTGTCTGATGCATCTGATGCGGC	308							
Qy	307	T---TGGCCTTCCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGAGCTG	363							
Db	309	TCGCTGGCGTGTGGTCTATTACTAGCCGCGGCGACCACTGGCCCTTCAGACACGGT	368							
Qy	364	CTCTGCAAGCTGTGTGCATCTCCTGTTTATATCAACCTTTACGGCAGCATCTGCTGCTG	423							
Db	369	CTCTGCAAGCTGTGTGCGCTTCTCTTCTACACCAACCTTTACTGCAGCATCTCTTCTCT	428							
Qy	424	ACCTGCATCTGTGTGCAACGAGTTCCTAGTGTGTGTGCCACCACTGTGTGTGCTGCCCTAC	483							
Db	429	ACCTGCATCAAGCTGACCGGTGTCTGGGCGCTTTAGACCTCTGCGCTCCGCTCGCTGG	488							
Qy	484	CGGACCCGCAAGCATGCTGTGCTGGCACCAAGCACCACTGGGCGCTGTGTGCTCTCCAG	543							
Db	489	GGCCGGGCCCGCTACGCTCGCCGGTGGCGGGCGGTGGG---TGTGTGGTGGCC	545							
Qy	544	CTGTGCCCAACTGGGCTTCTCCCAACGGACTACATCAATGSCCAAGATATCTGGTAT	603							
Db	546	TGCCAGGCGCCCGTGTCTACTATTGTTCACCAACAGCGCGCGCGCGCTAAACCTGCCAC	605							
Qy	604	GACATGACCAAGCAAGAGATTTTGATCGGGCTTTTGCCCTACGGCATAGTCTGACATTG	663							
Db	606	GACACTCGGACCCGAGCTCTTCAGCCGCTTGTGGCCTACAGCTAGTCATGCTGGGC	665							
Qy	664	TCTGGCTT---TCTTTCCCTCTTGCTCATTTTGGTGTCTATTCACTGATGGTCAGGAGC	721							
Db	666	CTGCTCTTCGGGGTGCCCTTGGCGTCACTCTTGTGTGTAGTGTCTATGGCTCGCGA	725							
Qy	722	CTGATCAAGCCAGAGGAACCTCATGAGGACAGGCAACAGCCCGGAGCCAGGTCTATC	781							
Db	726	CTGTAAAGCCAGCCTACGGACCTCGGGGCGCTGCTGATGGGCGCAACGCAATGCTGGT	785							
Qy	782	CGGACCATCTACTGGTGTGGGCTCTTCAACCCTGTGTTTGTGGCCCTTCCATATCACT	841							
Db	786	CGCACCATCGCCGTGGTGTGGCTCTTTCGCCCTCTGCTTCTGTGCCATTCCAGTCAAC	845							
Qy	842	CGTCTCTTACCTTCAACACTGTGTTTCTGTGTTTCTCAGGACTGCGCAGCTCTTGATGCA	901							
Db	846	CGCACCCCTTACTACTCTTCCGCT---CGCTGGACCTCAAGTGTGCCACACCCCTCAAAGCC	902							
Qy	902	GCCAGTGGGCTACAGATATGAGGCTCTCTGTGTGAGTGTGACAGCTGCTCAACCCA	961							
Db	903	ATCAACATGGCTCAAGAGT---TACCGGCTGGCCAGTGTAAAGTGTGCTTGAACCCC	959							
Qy	962	GTCTGTACTTCTTTCAAGG	982							
Db	960	GTGCTCTACTCTCTGGCTGGG	980							

RESULT 6
US-09-016-434-1068
; Sequence 1068, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Jaacie Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MG-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1068:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1124904
9-016-434-1068

Query Match	16.5%;	Score 178.6;	DB 4;	Length 1429;
Best Local Similarity	54.0%;	Pred. No. 2.1e-39;		
Matches 481;	Conservative 0;	Mismatches 394;	Indels 16;	Gaps 5;
QY	126	CTGCCAGTTCTCAGAGAAGTCACAAGAGCTCTACCTCTCTCCCTGGCTACAGTATCATCTTT	185	
Db	258	CTGTTGGTTTGATGAGATTTCAGATTTCATCTCTGCTGCCTGTGAGCTATGCAGTTGTCTTT	317	
QY	186	TATCTTAGGCTGCCACTAAATGGCACTGCTTTGTGGCACTCTCTGGGCGCAACCAACGACG	245	
Db	318	TGTCGTGGGCTTGGGCTTTAAACCCCAACCCCTATGGCTCTTCATCTTCGCCCTCCGACC	377	
QY	246	CTGGAGCTGTGCCACCACCTATCTGCTGAACCTGATGGTGGCGGACCTGCTTTATGTGCT	305	
Db	378	CTGGATGCAACGGCCACCTACATGTTTCCACCTGGCATTGTCAAGACACCTTGTATGTCT	437	
QY	306	AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGAGCT	362	
Db	438	GTGCTGCCCAACCTCATCTACTATTATGAGCCCAACCACTGGCGCCCTTTGGCACTGA	497	
QY	363	GCTCTGCAAGCTGGTGCACCTTCTGTTTCTATATCAACCTTTAGCGGAGCATCTCTGCTGCT	422	
Db	498	GATCTGCAAGTTCGTCGGCTTCTTTTCTATTGGAACCTCTACTGCACTGCTCTTTTCT	557	
QY	423	GACTGCATCTCTGTGCAACAGTTCTCTAGTGTTGTGGCACCCCACTGTGCTGGTCCCTTA	482	
Db	558	CACCTGCATCAGCGTGCACCGCTACCTGGGCACTGTCCACCCACTTCGGGCACCTACGCTG	617	
QY	483	CCGGACCCGAGCATGCTGGCTGGGCAACCAAGCACCTCTGGCGCCCTGCTGGTCTCCCA	542	
Db	618	GGGCGGCCCTCGCCTCGCAGGCTTCTCTGCTGGGCAAGTTGTTGGTCTGACCGGCTG	677	
QY	543	CTGCTGGCCCACTGGGCTTTCTCCACACGGACTACATCAATGGCCAGATGATCTGGTA	602	
Db	678	CTCTGTGCCCAACCTGTTCTTTGTTCACACCAAGCAACAAAGGACCAACCGTCTGTGCCA	737	


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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/513,974B
  FILING DATE: 14-SEP-1995
  CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/JP95/01599
    FILING DATE: 10-AUG-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 7-093989
    FILING DATE: 19-AUG-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 7-057186
    FILING DATE: 16-MAR-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 7-007177
    FILING DATE: 20-JAN-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-326611
    FILING DATE: 28-DEC-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-270017
    FILING DATE: 02-NOV-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-236357
    FILING DATE: 30-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-236356
    FILING DATE: 30-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-189274
    FILING DATE: 11-AUG-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-189273
    FILING DATE: 11-AUG-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 6-189272
    FILING DATE: 11-AUG-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Resnick, David S.
    REGISTRATION NUMBER: 34,235
    REFERENCE/DOCKET NUMBER: 45753
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617-523-3400
      TELEFAX: 617-523-6440
    INFORMATION FOR SEQ ID NO: 57:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 984 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
        MOLECULE TYPE: cDNA
  US-08-513-974B-57

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Query Match 15.2%; Score 164.8; DB 3; Length 984;
Best Local Similarity 52.0%; Pred. No. 1.1e-35;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

Qy 126 CTGCGAGTCTCAGAGAGTACAGCAAGTCACTCTCCCTGCGCTACAGATATCATCTT 185
Db 51 CTGTGTCTACCGGAGCACTTCAAGCAACTGCTGCTCCCACTGTGTATTCGGGGTGT 110
Qy 186 TATCCTAGGGGTGCCACTAAATGGCACTGTCTTGTGGCACTCTCTGGGGCCAAACCAAGCG 245
Db 111 GGCGGCTGGCGTCCGCTGAACATCTGTGTCATTAACCAAGTCTGACGTCGCCGGGC 170
Qy 246 CTGAGCTGTGCCACCACTTATCTGGTGAACCTGATGCTGGCGCACTGCTTTATGTGCT 305
Db 171 CCTGACCGGACGCGCGGTGTACACCCCTTAAACCTTGTCTGCTGACCTGTATATGCTG 230
Qy 306 AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 362
Db 231 CTCCTGCCCTGTCTCACTACACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 290

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RESULT 9

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US-09-461-436B-57
; Sequence 57, Application US/09461436B
; Patent No. 6538107
; GENERAL INFORMATION:
; APPLICANT: Shuji Hinuma
; Ryo Fujii
; Yasuaki Ito
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwards & Angell, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>

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Qy 363 GCTCTGCAAGTGTGTGCACTTCTCTGTATATCAACCTTTACGGCAGCATCTCTGCTCT 422
Db 291 CGCCTGCGCGCTGTGTGCGCTTCTCTCTATATGCCAACTGTCAGCGCAGCATCTCTTCT 350
Qy 423 GACCTGCACTCTGTGTGCAAGTCTCTAGTGTGTGTCACCACTGTGTGCTGCTGCTCA 482
Db 351 CACCTGCATCAGCTTCCAGCGCTACCTGGGATCTGCGCCAGCTGCGCCCTGCGCAAA 410
Qy 483 CC---GGACCCCGCAGGCATGCTGTGCTGGGCAACCAAGCACTTGGGGCTGTGCTGCT 539
Db 411 AGTGTGGGGCGCGCGCTGCTGTGTGTGTAACTGCTGTGCTGGCTGGCGTGTGCAAC 470
Qy 540 CCAGTGTGCTGCGCACTGCGCTTCTCCACAGGACTACATCAATGCGCAGATGATCTG 599
Db 471 CCAGTGTGCTGCGCACTGCGCTTCTGCTGCCACAGCATCTTCTGCTGCCACAGCATCC 530
Qy 600 GTATGACATGACCAAGCAAGAGATTTTGTATCGGCTTTTGTGCTACCGCATAGTTCTG 659
Db 531 CTATGACCTCAGCCCGCTGCTGCTGCCACCACTATATGCTTATGCGCATGGCTTCTC 590
Qy 660 ATTGTCTGGCTTCT--TTCCCTCTCTGTGCTATTTGTGTGCTATTCAGTATGGTCA 717
Db 591 TGTCTATCGGCTTCTGCTGCGCTTGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
Qy 718 GAGCTGATCAAGCCAGAGGAGAACTCATGAGGACAGGCAACAGCCCGAGCGCAGGTC 777
Db 651 CGCCTGTGCGCGCAGGATGCGCGCAGAGCTGTGCGCCAGGAGCGCGGTGGCAAGGC 710
Qy 778 CATCCGGACCATCTCTACTGCTGTGTGCGCTCTTCAACCTCTGTTTTGTGCGCTTCC 837
Db 711 GCGCCGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 838 CACTGCTCTCTTACTACTCACTGCTGCTTCTGCTTCTGCTTCTCAGGACTGCGACTTGT 897
Db 771 CACCAAGACAGCTTACCTGCGCAGTGGCTGCGCGCGGCTGCGCTGCTGCTGCTGCT 830
Qy 898 GCGAGCCAGTGTGCGCTTACAGATATGAGGCGCTCTGCTGAGTGTGAGCAGTGGCTCAA 957
Db 831 GCGCTTTCAGCGGCTTACAGGCAACGCGCGCGCTTTCAGTGTGCAACAGCGTGTGGA 890
Qy 958 CCCAGTCTCTGCTACT 971
Db 891 CCGCATCTCTTCT 904

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>

REFERENCE/DOCKET NUMBER: 45753 DIV2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 57:

US-09-461-436B-57

Query Match 15.2%; Score 164.8; DB 4; Length 984;
Best Local Similarity 52.0%; Pred. No. 1.1e-35;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

QY 126 CTGCAGTCTCAGAGAGTCAAGCAAGTCTACTCTCCCTGGCCCTACAGTATCATCTT 185
DB 51 CTGTGTCTACCGCGAGAACTTCAAGCAACTGCTGCTGCCACTGTGTATTGCGCGTGT 110
QY 186 TATCTAGGCTGCCACTAAATGCACTGTCTTGTGGCACTCTCTGGGGCCAAACCAAGCG 245
DB 111 GCGGCTGCTGCGCTGCGTGAACATCTGTGTGATTAACCAAGTCTGACGTCCCGCGGCG 170
QY 246 CTGAGCTGTGCCACCACTATCTGTGTAACCTGATGCTGGCGCACTGTTTATGTGCT 305
DB 171 CTTGACCGCGCGCGGTGACACCCCTAAACCTTGTCTGTGCTGACCTGATATGCTG 230
QY 306 AT---TGCCCTCTCATCATCACTACTACTAGATGACAGTGGCCCTTCGGGAGCT 362
DB 231 CTCCTGCCCCCTGTCTCATCTCACTATGCCAAGGTGATCCTGGCCCTTTGGCGACTT 290
QY 363 GCTCTGAAGTGTGTGCACTTCTCTTCTATATCAAGCTTTACGGCAGCATCTCTGTGCT 422
DB 291 CGCCTGCGCGTGTGCTGCTCTCTCTTCTATGCCAAGTGTGCAAGTGTGCTGCTTCTCT 350
QY 423 GACCTGATCTCTGTGACCAAGTCTCTAGTGTGTGCAAGTGTGCTGCTGCTGCTGCT 482
DB 351 CACCTGATCATGCTTCCAGCGCTACCTGGGATCTGCCACCGCTGGCCCTTCGGACAA 410
QY 483 CC---GGACCGCGAGGATGCTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
DB 411 ACGTGGGGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470

QY 540 CCAGCTGTGCTGCCACACTGGCTTCTCCACACGAGCTACATCAATGCCAGATGATCTG 599
DB 471 CCAGTGTGCTGCCACAGCACTTCTGCTGCCACAGGATCCAGGATCAACCGACTGTCTG 530
QY 600 GTATGATGACCAAGCAAGAGATTTTGTATGGGCTTTTTCCTACGCGATAGTCTGAC 659
DB 531 CTATGACCTCAGCGCGCTGCTGCCACCACTATATGCCCTATGCGATGGCTCTCAC 590
QY 660 ATTGTCTGCTTCT--TTCCCTCTCTGCTCAATTTTGTGTGCTTATTCATGATGCTCAG 717
DB 591 TGTATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
QY 718 GAGCTGTATCAAGCAGGAGGAACTCATGAGGACAGCAACACAGCCCGAGCGAGTCT 777
DB 651 CGGCTGTGCGCGCAGGATGCGCGGCGAGAGCTGTGCGCCAGGAGCGCGCTGCAAGGC 710
QY 778 CATCGGACCATCTACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
DB 711 GCGCGCATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
QY 838 CACTGCTCTTCTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
DB 771 CACCAAGACAGCTTACCTGCGAGTGGGCTGCAACGCGCGGCTGCTGCTGCTGCTGCTG 830
QY 898 GCGAGCAGTGTGCGCTACAGATATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
DB 831 GCGCTTTCAGCGGCTTCAAGGACGCGCGCTTTCAGTGTGAGTGTGAGCAGCTGCTCAA 890
QY 958 CCCAGTCTCTTACT 971
DB 891 CCCCATCTCTCT 904

RESULT 10

US-08-513-974B-379
; Sequence 379, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ogi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 379:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1023 base pairs
 TYPE: nucleic acid
 TOPOLOGY: double
 STRANDEDNESS: double
 MOLECULE TYPE: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 37..1020
 US-08-513-974B-379

Query Match 15.28; Score 164.8; DB 3; Length 1023;
 Best Local Similarity 52.08; Pred. No. 1.2e-35;
 Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;
 126 CTGCGAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 185
 87 CTGTGCTACCGGAGAACTCAAGCAACTGCTGCTGCCACCTGTGTATTGGCGGTGCT 146
 186 TATCCTAGGGTGCACATAATGACACTGTCTTGTGCACTCTCTGGGCCAAACCAAGCG 245
 147 GCGCGCTGGCTGCGCTGCAACATCTGTGTATACCAAGATCTGCACGTCCCGCGGGC 206
 246 CTGAGAGTGTGCCACCACTATCTGTGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCT 305
 207 CCGAGCCGACGCGCGGTGTACACCTTAACCTTGTCTGCTGACCTGCTATATGCGCTG 266
 306 AT---TGGCCCTTCTATATATACCTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 362
 267 CTCCTGCGCCGTCTATCTACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 326
 363 GCTCTGCAAGTGTGCTGCTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCT 422
 327 CGCTGCGCGCTGCTGCTTCTTCTTCTATGCAACCTGCAACGGCAGCATCTCTTCTCT 386
 423 GACCTGATCTCTGTGACCAAGTTCCTAGGTGTGTGCAACCACTGTGTTGCTGCGCTA 482
 387 CACCTGATCAGCTTCCAGCGCTACCTGGGATCTGCAACCGCTGGCCCTGGGCAAA 446
 483 CC---GGACCCGAGGATGCTGGTGGGACACGACCACTGGGCCCTGGTGGTCT 539

RESULT 11
 US-09-016-434-1108
 ; Sequence 1108, Application US/09016434
 ; Patent No. 6500936
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1108:

Db 447 ACGTGGGGCGCGCGGCTGCTTGGCTAGTGTGTGTAAACCGTGTGGCTGGCGGTGACAAC 506
 Qy 540 CCAGCTGCTGCCACACTGGGCTTCTCCACACGGAATACATCAATGCGCCAGATGATCTG 599
 Db 507 CCAGTGTGCTGCCACAGCCATCTTCGCTGCCACAGGATCCAGCGTAAACCGCACTGCTG 566
 Qy 600 GTATGACATGACAGCCAGAGAAATTTTGTATCGGCTTTTCCCTACGGCATAGTTCTGAC 659
 Db 567 CTATGACCTCAGCCCGCTGCGCTGGCCACCACTATATGCCCCTATGGCATGGCTCTCAC 626
 Qy 660 ATTGCTGCGCTTCT--TTCCCTCCTTGGTCAATTTTGGTGTGCTTATTCACATGATGGTCA 717
 Db 627 TGTATCGGCTTCTGCTGCGCTTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
 Qy 718 GAGCCTGATCAAGCCAGAGAGAACCTCATGAGACAGGGAACACAGCCCGAGCGAGTCT 777
 Db 687 CGGCTGTGCGCCAGGATGCGCGGAGAGCTGTGCGCCAGGAGCGCGCTGGCAAGGC 746
 Qy 778 CATCGGACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
 Db 747 GCGCGCATGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 806
 Qy 838 CACTGCTCTTCTTACCTCAACATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 897
 Db 807 CACCAAGACAGCTTACCTGGGCTGCGAGTGGGCTGCGAGCGCGGCGTCCCTGCACTGTATTGA 866
 Qy 898 GCGACCCAGTGGCTTACAAGATATGAGAGCTCTGAGAGCTCTGAGTGTGAGCAGCTGCTCAA 957
 Db 867 GCGCTTTGAGCGGCTTACAAAGCAGCAGCGCGCTTTGCCAGTCCCAACAGCGTCTGGA 926
 Qy 958 CCGAGTCTCTTACT 971
 Db 927 CCGCATCTCTTCT 940

SEQUENCE CHARACTERISTICS:
LENGTH: 1571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1296659
US-09-016-434-1108

Query Match 15.1%; Score 163.2; DB 4; Length 1571;
Best Local Similarity 51.9%; Pred. No. 3.9e-35;
Matches 443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;

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QY 126 CTGCGAGTCTCAGAGAGTACAGAGAGTCTCTCCCTGCGCCCTACAGATATCATCTT 185
DB 126 CTGCGAGTCTCAGAGAGTACAGAGAGTCTCTCCCTGCGCCCTACAGATATCATCTT 185
QY 327 CTGTGTCTACCGCGAGAGACTTCAAGCAACTGCTGTCACCTGTGATTCCGGCGTGT 386
DB 327 CTGTGTCTACCGCGAGAGACTTCAAGCAACTGCTGTCACCTGTGATTCCGGCGTGT 386
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DB 186 TATCTAGGCTGCCACTAAATGGCACTGCTTGTGGCACTCTCGGGCCCAACCAAGCG 245
QY 397 GCGGCTGGCTGCGCTGGAACATCTGTGTCAATTACCCAGATCGACGTCGCCCGGCG 446
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QY 567 CGCTGCGCGCTGTGCGTCTCTTCTATGCAACCTGCAAGGAGATCTCTTCTCT 626
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DB 627 CACCTGATCACTTCCAGCGCTACCTGGGCACTGCGCCGCTGGCCCGCTGGCACA 686
QY 483 CC---GGACCGCAGGATGCTGCTGGCGGCAACCACTGCGCCCTGCTGCTCT 539
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QY 747 CCAGTGTGCTGCCACAGCCATCTTCTGCTGCGCAGAGGATCCAGCGTAACCGCACTGCTG 806
DB 747 CCAGTGTGCTGCCACAGCCATCTTCTGCTGCGCAGAGGATCCAGCGTAACCGCACTGCTG 806
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DB 718 GAGCTGATCAAGCAGAGAGAGACCTATGAGAGACAGGCAACACAGCCCGCAGGCTG 777
QY 927 CCGCTGTGCGCCAGGATGCGCCGAGAGCTGTGGCCCGCAGGCGCGCTGGCAGGCG 986
DB 927 CCGCTGTGCGCCAGGATGCGCCGAGAGCTGTGGCCCGCAGGCGCGCTGGCAGGCG 986
QY 778 CATCCGACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
DB 778 CATCCGACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
QY 987 GCGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
DB 987 GCGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
QY 838 CACTGCTCTCTTCTACTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
DB 838 CACTGCTCTCTTCTACTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
QY 1047 CACCAAGACAGCTTACCTGTCAGTGTGCTGCAAGCCCGGCGCTGCTGCTGCTGCTGCT 1106
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QY 898 GGCAGCCAGTGTGCTTACAGATATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
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QY 1107 GGCCTTTGAGCGGCTCTCAAGGACGCGGCGCTTTTGCCAGTGGCCAAAGCGGTGCTGGA 1166
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QY 958 CCCAGTCTCTGACT 971
DB 958 CCCAGTCTCTGACT 971
QY 1167 CCCCATCTCTCTCT 1180
DB 1167 CCCCATCTCTCTCT 1180
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RESULT 12

US-08-459-046-1
Sequence 1. Application US/08459046
Patent No. 6008039
GENERAL INFORMATION:

APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: A No. 6008039el Human Purinergic P2U Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 Hillview Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,046

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0038 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: Placenta
CLONE: 179696

US-08-459-046-1

Query Match 14.5%; Score 156.8; DB 3; Length 984;

Best Local Similarity 51.4%; Pred. No. 1.8e-33;
Matches 439; Conservative 0; Mismatches 407; Indels 8; Gaps 3;

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QY 126 CTGCGAGTCTCAGAGAGTACAGAGAGTCTACTCTCCCTGCGCCCTACAGATATCATCTT 185
DB 126 CTGCGAGTCTCAGAGAGTCTCAGAGAGTCTACTCTCCCTGCGCCCTACAGATATCATCTT 185
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DB 111 GCGCGCTGCCCTCCCGCTGAAACATCTGTGTCAATACCCAGATCTGCAGCTCCCGCGGC 170
QY 246 CTGAGAGTGTGCCACCACTATCTGGTGAACCTGATGCTGGCGCCGACCTGCTTTATGTCT 305
DB 246 CTGAGAGTGTGCCACCACTATCTGGTGAACCTGATGCTGGCGCCGACCTGCTTTATGTCT 305
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DB 171 CTTGACCGCAGCGCGGTGTGTACACCTTAACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 230
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DB 306 AT---TGCCCTTCTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGAGCT 362
QY 231 CTCCTGCTGCCCTGCTCATCTAACTATGCAAGGTGATCACTGGCGCTTTGGCGACTT 290
DB 231 CTCCTGCTGCCCTGCTCATCTAACTATGCAAGGTGATCACTGGCGCTTTGGCGACTT 290
QY 363 GCTCTGAGAGTGTGCACTTCTCTCTGTTCTATATCAACTTTACGGCAGCATCTCTGCTGCT 422
DB 363 GCTCTGAGAGTGTGCACTTCTCTCTGTTCTATATCAACTTTACGGCAGCATCTCTGCTGCT 422
QY 291 CGCCTGCGCGCTGCTGCTGCTTCTTCTATGCAACCTGCAAGGAGATCTCTTCTCT 350
DB 291 CGCCTGCGCGCTGCTGCTGCTTCTTCTATGCAACCTGCAAGGAGATCTCTTCTCT 350
QY 423 GACCTGCACTCTCTGTGCAACCACTTCTAGGTGCTGCGCACCCACTGTGCTGCTGCTGCTGCT 482
DB 423 GACCTGCACTCTCTGTGCAACCACTTCTAGGTGCTGCGCACCCACTGTGCTGCTGCTGCTGCT 482
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Db 351 CACCTGCATCAGCTTCACAGCGCTACCTGGGCACTGCGCACCCGCTGGCCCTGGCAAA 410
Qy 483 CC---GGACCCGAGGATGCCCTGGCTGGGCAACAGCAACACCTGGCCCTGGTGTCT 539
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Qy 540 CCAGCTGCTGCCACACAGCTGCTTCCACACGGACTACATCAATGGCCAGATGATCTG 599
Db 471 CCAGTGCCTGCCACACAGCTTTCCTGCCACAGGATCCAGGTAACCGCACTGCTG 530
Qy 600 GTATGACATACACAGCAAGAGAAATTTGATGCGCTTTTGGCTACCGGATGATCTGAC 659
Db 531 TTATGACCTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
Qy 660 ATTGCTGGCTTCT---TTCCCTCTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
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Qy 718 GAGCTGATCAAGCAGGAGAGAACTCATGAGACAGGCAACACAGCCCGAGCCAGGTC 777
Db 651 CCGCTGTGCGCGCAGGATGCGCGGCGAGAGCTGTGGCCAGGAGCGGGTGGCAAGGC 710
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Db 711 GCGCCGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 838 CACTCGCTCTCTTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCGCAGCTCTTGAT 897
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Qy 898 GGCAGCCAGTGTGGCTTACAGATATGAGGCTCTGCTGAGTGTGAGGAGCTGCTCAA 957
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Qy 958 CCCAGTCTGTACT 971
Db 891 CCCATCTCTTCT 904

RESULT 13

US-09-102-710B-1
; Sequence 1, Application US/09102710B
; Patent No. 6479630
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PP-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6479630 179696CB1
US-09-102-710B-1

Query Match 14.5%; Score 156.8; DB 4; Length 984;
Best Local Similarity 51.4%; Pred. No. 1.8e-33;
Matches 439; Conservative 0; Mismatches 407; Indels 8; Gaps 3;
Qy 126 CTGCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 185
Db 51 CTGTGCTTACCGGAGACTTCAAGCACTGCTGCTCCCACTGCTGATTTCGGGGTGTCT 110
Qy 186 TATCTAGGCTGCCACTAATGACATGCTTGTGGCACTCTCTGGGCGCCAAACCAAGCG 245
Db 111 GCGCGCTGCCCTCCCGCTGAACATCTGTGTCATTACCCAGATCTGCACTCCCGCGGGC 170

Qy 246 CTGGAGCTGTGCCACCACTATCTGTTGAACCTGATGTTGGCCGACCTGCTTTATGTCT 305
Db 171 CTTGACCCGAGGCGGTGTACACCCCTAAACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 230
Qy 306 AT---TGCCCTTCTTCATCATCACTACTACTAGATACAGGTTGGCCCTTCGGGGAGCT 362
Db 231 CTCCTGCCCCCTGCTCATCTACAACTATGCGCAAGGTGATCACTGGCCCTTTGGCGACTT 290
Qy 363 GCTCTGCAAGCTGGTGCACTTCTCTTCTATATCAACCTTTACGCGACATCTCTGCTCT 422
Db 291 CGCCTGCGCGCTGGTCCGCTTCTCTTATGCGCAACCTGACGGGAGATCTCTTCTCT 350
Qy 423 GACCTGCATCTCTGTGCAACCACTTCTAGTGTGTGCGCACCACTGTGTTGCTGCTCTA 482
Db 351 CACCTGCATCAGTTCAGCGCTACTGCGCATCTGCCACCGCTGGCCCTGCGCCACAA 410
Qy 483 CC---GGAACCCGCGAGGATGCTGCTGGCGCACCGACCACTGGGCGCTTGGTGTCT 539
Db 411 AGTGGGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
Qy 540 CCAGCTGTGCGCCACACTGGCCTTCTCCACACGAGCTACATCAATGGCCAGATGATCTG 599
Db 471 CAGTGTGCTGCGCCACAGCACTTCTGCTGCCACAGGATCCAGCGTAACCGCACTGTCTG 530
Qy 600 GTATGACATGACCAAGCAAGAAATTTGATGCGCTTTTGGCTTACGGCATAGTCTGAC 659
Db 531 TTATGACCTCAGCCCGCTGCGCTGCGCACCCACTATATGCCCTATGGGATGGCTCTCAC 590
Qy 660 ATTGCTGGCTTCT---TTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Db 591 TGTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
Qy 718 GAGCTGTATCAAGCCAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCGAGTCT 777
Db 651 CCGCTGTGCGCCAGGATGCGCGGCGAGAGCTGTGGCCAGGAGCGCGTGGCAAGGC 710
Qy 778 CATCGGACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
Db 711 GCGCCGATGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 770
Qy 838 CACTGCTCTCTTCTACCTCACCATCTGCTTCTGCTTCTCAGGACTGCGCAGCTCTTGAT 897
Db 771 CACCAAGACGCTTACTGCGAGTGCCTCGACGCGCGGGCTGCCCTGCACTGTATTGA 830
Qy 898 GGCAGCCAGTGTGGCTTACAGATATGAGGCTCTGCTGAGTGTGAGGAGCTGCTCAA 957
Db 831 GGCCTTTGCGAGCGCTTACAAAGCACGCGCGCTTTGCGCAGTGCCTGCAACAGCGTGTGA 890
Qy 958 CCCAGTCTGTACT 971
Db 891 CCCATCTCTTCT 904

RESULT 14

US-08-513-974B-41
; Sequence 41, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ontaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ogi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-461-436B-41

Query Match 13.8%; Score 148.8; DB 4; Length 984;
Best Local Similarity 50.8%; Pred. No. 2.9e-31;
Matches 434; Conservative 0; Mismatches 412; Indels 8; Gaps 3;
Qy 126 CTGCCAGTCTCAGAGAGTACAGCAAGTCACTCTCCCTGGCCTACAGTATCATCTT 185
Db 51 CTGGCTCTACCGTGGAGATTCAAGCACTCTCTAACCCTGGTATCTCGGTGGTCT 110
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Db 111 GGTGGTGGCTGCCACTGAACATCTGGTCACTGGCCAGATCTGGCATCCCGCCGGAC 170
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Qy 423 GACCTGCATCTCTGTGCACCACTGCTTAGGTGTGTGCCACCACTGCTGTTCGCTGCCCTA 482

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Job time : 116 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 08:39:02 ; Search time 3904 Seconds
(without alignments)
10099.331 Million cell updates/sec

Title: US-10-763-972-1
Perfect score: 1082
Sequence: 1 atgcgtccatttgcctcc.....ccagggttgacagatctgg 1082

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_est8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.6	18.5	2542	3	AK017378 Mus muscu
2	200.6	18.5	3001	3	AK005013 Mus muscu
3	177.6	16.4	693	6	CD217676 Dgln.pk0
4	163.2	15.1	987	9	AY400797 Homo sapi
5	163.2	15.1	1425	3	CR624871 full-leng
6	163.2	15.1	1515	3	CR612681 full-leng
7	163.2	15.1	1532	3	CR618945 full-leng
8	163.2	15.1	1564	3	CR626266 full-leng
9	163.2	15.1	1589	3	CR626754 full-leng
10	163.2	15.1	1592	3	CR605588 full-leng
11	163.2	15.1	1594	3	CR608834 full-leng
12	163.2	15.1	1638	3	CR617080 full-leng
13	163.2	15.1	1651	3	CR597500 full-leng
14	163.2	15.1	1686	3	CR626706 full-leng
15	163.2	15.1	1690	3	CR598765 full-leng
16	161.8	15.0	925	5	EX704227 BX704227
17	158.8	14.7	4439	3	AK076364 Mus muscu
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19	148.8	13.8	987	9	AY400799 Mus muscu
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21	141.2	13.0	641	5	BQ396255 NISC tg19
22	141.2	13.0	1090	5	BX397648 BX397648
23	140.2	13.0	627	1	AL675845 AL675845
24	140.2	13.0	1168	1	AL561864 AL561864

ALIGNMENTS

RESULT 1	AK017378	2542 bp	linear	HTC 03-APR-2004
LOCUS	Mus musculus	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430432J15 product:PURINERGIC RECEPTOR P2Y,		
DEFINITION	G-PROTEIN COUPLED 2, full insert sequence.			
ACCESSION	AK017378	GI:12856588		
VERSION	AK017378.1	HTC; CAP trapper.		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research			

C	25	140	12.9	1023	5	BX332649	BX332649
	26	134.8	12.5	1815	7	CN210812	RJA041C08
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	30	128.2	11.8	899	5	BQ591110	AGENCOURT
C	31	127.2	11.8	1095	5	BX358251	BX358251
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QY 782 CGGACCATCTACTGCTGTGGGCTCTTACCTCTGTTTGTGGCTTCCATATCACT 841
Db 1209 CGACCATGCTGTGTACTGGCTCTTCCCTCTGCTCTGCTTCTTCCCTCAG 1268
QY 842 CGCTCCTTCTACTCACCATCTGCTTTCTGCTTCTCAGGACTCCAGCTTTGATGGCA 901
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QY 902 GCCAGTGGGCTCAAGATATGGAGGCTCTGCTGTGAGTGAGCAGCTGCCCAACCCA 961
Db 1326 ATCAACATGGATATAGATCACCGGCGCTGCCAGCCCAACAGTTGCTTGGCCG 1385
QY 962 GTCCTGTACTTTCTTCAAG 982
Db 1386 GTACTCTACTTCTTGGCAGG 1406

RESULT 3
CD217676
LOCUS
DEFINITION
693 bp mRNA linear EST 20-MAY-2003
pgln.pk004.g6 Normalized chicken reproductive tract cDNA library
(sp|J09807|P2V3_CHICK_P2V3_purinoceptor_3_(P2Y3)(Nucleoside
diphosphate receptor) >emb|CA66930.1|(X95283) G protein-coupled
P2 receptor (Gallus gallus), mRNA sequence.
CD217676
ACCESSION
CD217676.1 GI:30957649
VERSION
EST.
KEYWORDS
Gallus gallus (chicken)
SOURCE
Gallus gallus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 693)
Cognburn, L.A. and Nys, Y.
Chicken ESTs from reproductive tract
Unpublished (2002)
Contact: Larry A. Cognburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cognburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
1..693
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/sex="Male and female"
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/dev_stage="Various stages; embryonic, post-hatch, immature
and sexually-mature"
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/clone_lib="Normalized chicken reproductive tract cDNA
library (pgln)"
/notes="vector: pCMVSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
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Best Local Similarity 59.2%; Pred. No. 4.2e-37;
Matches 359; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

QY 127 TGGCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTT 186
Db 67 TGCACCTTCATGAGAAATTCAGCAGGTCTGCTGCCCTGTCTACTCAGTGTGTTC 126
QY 187 ATCTAGGGCTCCACTAAATGGCACTGTCTTGTGGCACTCCCTGGGGCCAAACCAAGGCG 246
Db 127 CTACTGGGCTGCCACTCAATGCCGTGTCTATGGCAGATCTGCTGGCCGCAAGCGG 186
QY 247 TGGAGTGTGCCACACCACTATCTGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCTA 306
Db 187 TTGACCCGCAACCACTATCTACATGCTGAACCTGGCCATGGCGGACCTGCTTTATGCTGC 246
QY 307 T---TGCCCTTCTCATCATCACTACTCAGTGTGAGATGACAGGTGGCCCTTCGGGAGCTG 363
Db 247 TCCCTCCCTCTCTCATCTAGCACTACACCAAGAGATTACTGGCCCTTTGGGACTTC 306
QY 364 CTCTGCAAGCTGGTGCATCTTCTGTTCTATATCAACCTTTTACGGCAGCATCTCTGCTG 423
Db 307 ACCTGCAAAATTCGTCGGCTTCCAGTTCTACACCAACCTGCACGGCAGCATCTCTTCTCTC 366
QY 424 ACCTGCATCTGTGCACCACTCTCTAGTGTGTGCCACCCACTGTGTTCCTGCTGCCCTAC 483
Db 367 ACCTGCATCAGCTCCAGGCTACATGGGATCTGCCACCCCTTGGCCCTGTGGCACA 426
QY 484 CGGACCCG---CAGGCATGCTGGCTGGGCAACCACTGCGGCTGGTGGTCTCTC 540
Db 427 AAGAAGGAAAGAGCTGACGTGGCTGTGTGTGCTGCGTGTGTTTCATGTCATGCC 486
QY 541 CAGCTGTGCTGCCACACTGGCTTCTCCACAGGACTACATCAATGGCCAGATGATCTGG 600
Db 487 CAGTGCCTGCCACACTTTGTCTTGGCTTCCACCGGACGACAGAGATTCGACATGTCTGC 546
QY 601 TATGACATGACAGCAAGAGAAATTTGATCGGCTTTTGTGCTACGGCATAGTTCTGCACA 660
Db 547 TATGACCTGAGCCCCCGGACCGCTCCACATCTTCCCTATGGCATCAGCTTGA 606
QY 661 TTGCTGCTGCTTCT--TTCCCTCTTGTCTATTTTGGTGTGCTATTTACTGATGCTAGG 718
Db 607 ATCAGCGGCTTCTGCTGCCCTTCGACCCATCCTGGGCTCTGCTACTGCGATGCGCCG 666
QY 719 AGCCTG 724
Db 667 ATCTCTG 672

RESULT 4
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LOCUS
DEFINITION
987 bp DNA linear GSS 15-DEC-2003
Homo sapiens P2RY6 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY400797
VERSION
AY400797.1 GI:39756786
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 987)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
REFERENCE
2 (bases 1 to 987)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

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TITLE									
JOURNAL									
COMMENT									
FEATURES									
source									
1. 987									
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/mol_type="genomic DNA"									
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ORIGIN									
Query Match 15.1%; Score 163.2; DB 9; Length 987;									
Best Local Similarity 51.9%; Pred. No. 4.1e-33;									
Matches 443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;									
Qy	126	CTGCCAGTTCTCAGAGAAGTACAGCAAGTCTACTCTCCTGGCCTACAGTATCATCTT	185						
Db	51	CTGTGTCTACCGCGAGAATTCAAGCAACTGCTGTGTGCCACTGTGTATTGCGGGTGCT	110						
Qy	186	TATCCTAGGCGTGCACCTAAATGGCACTGTCTTGTGGCACTCTTGGGGCCAAACAACGC	245						
Db	111	GGCGGTGGCCTGCGGTGAACATCTGTGTATTACCCAGATCTGCAGTCCGCGCGGC	170						
Qy	246	CTGAGCTGTGCCACCACTATCTGTGTGAACCTGATGTGGCCGACCTGCTTTATGTGCT	305						
Db	171	CTTGACCGCGACGGCGGTGTACACCCTAAACCTTGCTGTGCTGACCTGCTATATGCGCTG	230						
Qy	306	AT---TGCCCTTCTCATCATCACTACTACTAGATACAGGTGGCCCTTTGGGGAGCT	362						
Db	231	CTCCCTGGCCCTGTCTCACTCAACTATGCCCAAGGTGATCACTGGCCCTTTGGCGACTT	290						
Qy	363	GCTCTGAAAGCTGTGTGCACTTCTCTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCT	422						
Db	291	CGCCTGCGCGTGTGTCGCTCTCTTCTATGCCAACCTGCACGCGCAGCATCTCTTCTCT	350						
Qy	423	GACCTGATCTCTGTGCACAGTTCCTAGTGTGTGTGCCACCACTGTGTTGCTGGCCCTA	482						
Db	351	CACCTGATCAGCTTCCAGCGCTACCTGGGCATCTGCCACCGCTGGCCCGCTGGCAAA	410						
Qy	483	CC---GGACCCGCGAGGATGCTGTGCTGGGCACCAAGCACCACTGGGCCCTGTGTGCTCT	539						
Db	411	ACGTGGGGCCCGCGGGCTGCTTGGCTAGTGTGTAGCCGTGTGGCTTGGCCGTGACAA	470						
Qy	540	CCAGCTGTGCCCACTATGGGCTTCTCCCAACGGACTACATCAATGGCCAGATGATCTG	599						
Db	471	CCAGTGCTGCCCAAGCCATCTTCGCTGCCACAGGCATCCAGCGCTAAACCGCACTGTCTG	530						
Qy	600	GTATGACATGACCCAGAGAGATTTTGTATCGGCTTTTTCCTACGCATAGTCTTCAC	659						
Db	531	CTATGACCTCAGCCGCGCTGCGCTGGCCACCACTATATGCCCCTATGGATGGCTCTCAC	590						
Qy	660	ATTGTCTGGCTTCTCT--TTCCCTCCTTGGTCAATTTTGGTGTGCTATTCACTGATGGT	717						
Db	591	TGTCATCGGCTTCTGTGCGCTTTTGCTGCCCTGCTGTGCCCTGCTACTGTCTCTGGCCTG	650						
Qy	718	GAGCCTGATCAAGCCAGAGAGAACCTCATGAGGACAGCCAAACAGCCCGAGCCAGGTC	777						
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Qy	778	CATCGGACCACTCTACTTGGTGTGGGCTCTTTCACCTCTGTTTGTGGCCCTCCATAT	837						
Db	711	GGCCCGCATGGCGTGGTGGTGTGCTGTGCCCTTGTCCATCAGCTTCTGCTTTTCACAT	770						
Qy	838	CACGTGCTCTTCTACCTCAACATCTGCTTTCTGCTTTCTCAAGACTGCCAGCTCTTGAT	897						
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Query Match      15.1%; Score 163.2; DB 3; Length 1564;
Best Local Similarity 51.9%; Pred. No. 4.6e-33;
Matches 443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;

QY 126 CTGCCAGTTCTCAGAGAAAGTACAGCAAGTCTACTCTCCCTGGCTACAGTATCATCTT 185
DB |||
DB 343 CTGTGTCTACCGGAGAACTTCAAGCAACTCTGCTGCCACTGTATTGGGGGTGCT 402
QY 186 TATCTAGGGTGCACATAAATAGGCACTGTTTGGCACTCTCTGGGGCCAAACCAAGG 245
DB |||
DB 403 GCGGCTGCGCTGCGCTGGAACATCTGTCTATTACCCAGATCTCGACGCTCCCGCGGC 462
QY 246 CTGGAGCTGTGCCACCACTATCTGTTGAACCTGATGTTGCCGACCTGCTTTATGTCT 305
DB |||
DB 463 CTGACCGCGACGCGCTGTACACCTTAACCTTGTCTGGCTGACCTGCTATATGCTG 522
QY 306 AT---TGCCCTTCTCATCATCACTACTCTAGATGACAGGTGGCCCTTGGGGAGCT 362
DB |||
DB 523 CTCCTGCGCTGCTCATCTACAATATGCCCAAGGTGATCACTGGCCCTTTGGCGACTT 582
QY 363 GCTCTGCAAGTGTGGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCTGCTGCT 422
DB |||
DB 583 CGCTGCGCTGCTGCTGCTCTTCTTATGCCAATCTGACGCGAGCATCTCTTCTCT 642
QY 423 GACCTGATCTCTGTGCAACCACTCTCTAGTGTGTGCCACCACTGTGTGCTGCCCTA 482
DB |||
DB 643 CACCTGATCACTGTCCAGCGCTACTTGGGCACTGTGCCACCGCTGCCCGCTGGCAAA 702
QY 483 CC---GGACCGCAGGCACTGCTGCTGGGCAACGACCACTGCGCCCTGCTGCTCT 539
DB |||
DB 703 ACGTGGGGCGCGCGCTGCTGCTGCTAGTGTGTAGCCGCTGTGCTGCGCGCTGACAAC 762
QY 540 CCAGCTGTGCGCCACCTCTCTCCCAACGCACTATCAATCAATGGCCAGATGATCTG 599
DB |||
DB 763 CCAGTGCCTGCGCCAGCCATCTTGGTGCACAGGCACTCAGCGTAAACCGCACTGCTG 822
QY 600 GTATGATGACACGACGCAAGAGAAATTTTATCGGCTTTTGGCTACGCGATAGTTCTGAC 659
DB |||
DB 823 CTATGACCTCAGCGCGCTGCGCTGGCCACCACTATATGCGCTTATGGCATGGCTCTCAC 882
QY 660 ATTGTCTGCTTCTCT---TTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
DB |||
DB 883 TGTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
QY 718 GAGCTGTATCAAGCAGGAGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTC 777
DB |||
DB 943 CCGCTGTGCGCGCAGGATGCGCGGCAAGAGCTGTGCGCCAGAGCGGCTGGCAAGGC 1002
QY 778 CATCGGACCACTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
DB |||
DB 1003 GGCCTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
QY 838 CACTGCTCTCTTCACTCACTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAT 897
DB |||
DB 1063 CACCAAGACAGCTTACCTGGCAGTGGCTGCAAGCGCGGCTGCTGCTGCTGCTGCTGCTG 1122
QY 898 GCGAGCCAGTGTGGCTTACAGATATGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 957
DB |||
DB 1123 GGCCTTTGACGCGCGCTTACAAAGGACGCGCGCGCTTTTGGCAGTGCCAAAGCGCTGCTGGA 1182
QY 958 CCCAGTCTGCTACT 971
DB |||
DB 1183 CCCCATCTCTTCT 1196

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RESULT 9
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 LOCUS
 DEFINITION
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 of Homo sapiens (human).
 CR626754
 VERSION
 CR626754.1 GI:50507616
 KEYWORDS
 HTC; CNSUT_cDNA.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1589)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
REMARK Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
REFERENCE 2 (bases 1 to 1589)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Location/Qualifiers
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ORIGIN
Query Match 15.1%; Score 163.2; DB 3; Length 1589;
Best Local Similarity 51.9%; Pred. No. 4.7e-33;
Matches 443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;

QY 126 CTGCCAGTTCTCAGAGAAAGTACAGCAAGTCTACTCTCCCTGGCTACAGTATCATCTT 185
DB |||
DB 382 CTGTGTCTACCGGAGAACTTCAAGCAACTCTGCTGCCACTGTGTATTGGGGGTGCT 441
QY 186 TATCTAGGGTGCACATAAATAGGCACTGTTTGGCACTCTCTGGGCAACCAAGCG 245
DB |||
DB 442 GCGGCTGCGCTGCGCTGCACTCTGTCTATACCCAGATCTGCACTGCCCGGCG 501
QY 246 CTGGAGCTGTGCCACCACTATCTGTTGAACCTCATGATGTTGGCGCACTCTTTATGCT 305
DB |||
DB 502 CTTGACCGCGCAGCGCGTGTACCCCTAAACCTTGTCTGCTGCTGCTGCTGCTGCTGCT 561
QY 306 AT---TGCCCTTCTCATCATCACTACTCTAGATGACAGGTGGCGCTTGGGGAGCT 362
DB |||
DB 562 CTCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
QY 363 GCTCTGCAAGTGTGGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCT 422
DB |||
DB 622 CCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
QY 423 GACCTGATCTCTGTGCAACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB |||
DB 682 CACCTGATCACTGCTTCCAGCGCTACTGCGGCACTGCGCCAGGCTGATCACTGCGCGCTTGGCGACTT 741
QY 483 CC---GGACCGCGCAGGCACTGCTGCTGCGCAACCACTGCGCGCTTGGGGAGCT 539
DB |||
DB 742 AGTGGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801
QY 540 CCAGCTGTGCGCCACACTGGCGCTTCTCCCAACGCACTATCAATGATGCGCAGATGATCTG 599
DB |||
DB 802 CCAGTGTGCGCGCCACAGCCATCTTGTGCTGCCAGGCACTCCAGCGTAAACCGCACTGCTG 861
QY 600 GTATGATGACACGACGCAAGAGAAATTTTATGCTGCTGCTTTCCTAGCGCATAGTTCTGAC 659
DB |||
DB 862 CTATGATCTCAGCGCGCTGCTGCTGCGCCACCACTATATGCTTATGCTGCTGCTGCTGCT 921
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[illegible]


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Db      655 CGCTGCGCGCTGCTCGCTTCTCTATATGCCAAGGTGATCACTGGGCCCTTTGCGGACTT 714
Qy      423 GACCTGCACTCTGTGCAACAGTCTCTAGGTGTGTGCCACCACTGTGTGCTGCGCTTA 482
Db      715 CACCTGCACTAGCTTCCAGCGCTTACCTTGGGATCTGCCACCGCTGCGCGCTGCGCAAA 774
Qy      483 CC---GGACCCGCGAGGATGCTGGCTGGGACACAGCACCACTGGCGCTGGTGTGCT 539
Db      775 ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTAGCGGTGGCTGGCGGTGACAAC 834
Qy      540 CCAGCTGCTGCCACACTGGCTTCTGCCACAGGACTPACATCAATGGCCAGATGATCTG 599
Db      835 CCAGTGCCTGCCACAGCATCTTCTGCTGCCACAGGATCCAGCGTAAACGCACTGTCTG 894
Qy      600 GTATGACATGACAGGCAAGAGATTTTGATCGGCTTTTGGCTGATCTACCTGATGTGAG 659
Db      895 CTATGACTCAGCGGCTGCGCTGGCCAGCACCACTATATGCCCCATGGCATGGCTCTCAC 954
Qy      660 ATTGTCTGGCTTCT--TTCCCTCCTTGGTGCATTTTGGTGTGCTATTACCTGATGTGAG 717
Db      955 TGTATCGGCTTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1014
Qy      718 GAGCTGATCAGCAGGAGAGACCTCATGAGACAGGCAACAGCCCGAGCGAGCTC 777
Db      1015 CCGCTGTGCGCGCAGGATGCGCGGAGAGCCCTGTGCGCCAGGCGGCTGGCAAGGC 1074
Qy      778 CATCGGACCATCTACTGTGTGTGGCTCTTTCACCTCTGTTTGTGGCTTCTCCATAT 837
Db      1075 GGCCCGCATGCGCTGTGTGGCTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 1134
Qy      838 CACTGCTCTCTTACCTACCATCTGCTTCTGCTTCTGCTTCTGAGACTGCGAGCTCTTGAT 897
Db      1135 CACCAAGACAGCTTACCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
Qy      898 GGCAGCAGTGTGCTACAGATATGAGGCTCTGCTGAGTGTGAGAGCTGCTGCTCAA 957
Db      1195 GGCCTTGTGAGGCTTACAAAGCACGCGGCGCTTTCAGAGTGCACAGCGTGTGGA 1254
Qy      958 CCCATCTGCTTACT 971
Db      1255 CCCATCTCTTCT 1268

RESULT 13
CR597500 full-length cDNA clone CS0DC005YM02 of Neuroblastoma Cot
LOCUS 25-normalized of Homo sapiens (human).
DEFINITION
ACCESSION CR597500 1651 bp mRNA linear HTC 21-JUL-2004
VERSION CR597500
KEYWORDS HT; CNSUT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1651)
Genoscope.
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

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end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen
FEATURES
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ORIGIN

Query Match      15.1%; Score 163.2; DB 3; Length 1651;
Best Local Similarity 51.9%; Pred. No. 4.7e-33;
Matches 443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;

Qy      126 CTGCCAGTCTTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTT 185
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Qy      186 TATCCTAGGGCTGCCACTAAATGGCACTCTCTTGTGGCACTCTCTGGGGCAACCAAGCG 245
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Qy      246 CTGGAGCTGTGCCACCACTATCTGTGTGAACCTGTATGTGTGGCGACCTGTCTTATGTGCT 305
Db      558 CTGACCCCGCAGGCGGTGTACACCTAAACCTGTCTGGCTGACCTGTCTATATGCTG 617
Qy      306 AT---TGCCCTTCTTCATCATCATCACTACTACTAGATGACAGTGGCCCTTCGGGAGCT 362
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Qy      363 GCTCTGCAAGCTGGTGCACCTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCT 422
Db      678 CGCCTGCGCCCTGGTCCGCTTCTCTTCTATGCCAACCTGCACGCGCAGCATCTCTTCT 737
Qy      423 GACCTGCATCTCTGTGCACAGTTCCTAGTGTGTGCCACCACTGTGTTCCTGCTGCTTA 482
Db      738 CACCTGCATCACTTCCAGCGCTACTGGGCACTGTGCCACCGCTGGCGCCCTGGGCAAA 797
Qy      483 CC---GGACCCGCGAGCATGCTGCTGGGCAACCAAGCACTCTGGCGCCCTCTGCTCT 539
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Qy      540 CCAGCTGTGCCCACTGCGCTTCTCCCAAGCACTATCAATATGGCCAGATGATCTG 599
Db      858 CCAGTGCCTTGGCCACAGCCATCTTCGCTGCCACAGGCACTCCAGCGTAACCGCACTGTCTG 917
Qy      600 GTATGACATGACAGCAGAGAGAAATTTTGATCGGCTTTTGGCTTACGGCATAGTCTGAC 659
Db      918 CTATGACCTCAGCGCGCTGCGCTGGCCACCACTATATGCGCTATGCGATGGCTCTCAC 977
Qy      660 ATTGTCTGGCTTCT--TTCCCTCCTTGGTCAATTTTGGTGTGCTATTCATGATGGTCA 717
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Qy      718 GAGCTGTATCAAGCAGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCGAGTCT 777
Db      1038 CCGCTGTGCCCGCAGGATGGCCCGGAGAGCTGTGGCCAGAGCGCGCTGGGCAAGGC 1097
Qy      778 CATCCGGACATCTTACTGGTGTGGCTCTTTCACCTCTGTTTGTGCTTGTCCATAT 837
Db      1098 GCGCCGATGCGCGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1157
Qy      838 CACTGCTCTTCTACCTCACCATCTGCTTCTGCTTCTCTGAGTCTCAGGACTGCGACTTGTAT 897
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Qy      898 GGCAGCCAGTGTGGCTTACAGATATGAGGCGCTCTGAGTGTGAGTGTGAGGCTGCTCAA 957
Db      1218 GGCCTTTCAGCGGCTTACAAAGGACGCGGCGCTTGCAGTGTGCCACAGCGTGTGGA 1277

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QY	958	CCAGTCTCTGACT	971
Db	1278	CCCCATCCTTTCT	1291
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LOCUS	full-length cDNA clone CS0DB006YE03 of Neuroblastoma Cot		
DEFINITION	10-normalized of Homo sapiens (human).		
ACCESSION	CR626706		
VERSION	CR626706.1 GI:50507568		
KEYWORDS	HTC; CNSLT cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1686)		
JOURNAL	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
REMARK	Full-length cDNA libraries and normalization Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope. 2 (bases 1 to 1686) Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
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	/tissue_type="Neuroblastoma Cot 10-normalized"		
	/plasmid="pCMVSPORT_6"		
ORIGIN			
Query Match	15.1%; Score 163.2; DB 3; Length 1686;		
Best Local Similarity	51.9%; Pred.No. 4.7e-33;		
Matches	443; Conservative 0; Mismatches 403; Indels 8; Gaps 3;		
QY	126	CTGCCAGTGTTTCAGAGAAGTCAACAAGTGTACCTCTCCCTGGCCCTACAGTATCATCTT	185
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QY	186	TATCTTAGGGTGGCACTAAATGGCACTGTCTTTGGCACTCTTGGGGCCCAACCAAGC	245
Db	524	GCGGGTGGCTTGGCGCTGAACATCTGTGTATTAACCAAGATCTGCACGTCCCCTGGGC	583
QY	246	CTGGAGCTGTGCCACCACTATCTGGTGAACCTGTATGTGGCGCACCTGTCTTTATGTCT	305
Db	584	CTGACCCGACGGCGGTGACACCTAACCCTTCTGCTGTGACCTGTATATGCTG	643
QY	306	AT---TGCCCTTCTCATCATCACTACTCATAGATGACAGGTGGCCCTTCGGGGAGCT	362
Db	644	CTCCCTGCCCTGCTCATCTACAACATATGCCAAGGTGATCACTGGCCCTTTGGCGACTT	703
QY	363	GCTCTGCAAGCTGGTGCATCTCCTGTCTATATAAACCTTTACGCGACATCTCTGCTCT	422
Db	704	CGCTGCCGCTGGTCCGCTTCTCTTCTATGCCAACTGTACGGCAGCATCTCTCTCT	763
QY	423	GACCTGCATCTCTGTGACACCACTTCTTAGGTGTGTGCCACCACTGTGCTTGCCTG	482
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/tissue type="Placenta Cot 25-normalized"
/Plasmid="PCWVSPORT_6"

ORIGIN

Query Match	15.1%	Score 163.2;	DB 3;	Length 1690;
Best Local Similarity	51.9%	Pred. No. 4.7e-33;		
Matches 443;	Conservative 0;	Mismatches 403;	Indels 8;	Gaps 3;

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Qy	186	TATCTAGGGTGGCCACTAAATGGCACTGTCTTGGCACTCTCTGGGCGCAAAACCAAGCG	245
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Qy	246	CTGAGCTGTGCCACCACTTACTCTGTGAACCTGATGGTGGCGCACTCTTTTATGTGCT	305
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Qy	306	AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT	362
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Db	704	CGCCTGGCGCTGGTCCGCTTCTCTTATATGCCAACCTTGCACGGCAGCATCTCTTCTCT	763
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Qy	483	CC---GGACCCGCGAGGATGCTGGCTGGGCAACAGCACCACTTGGGCGCTTGGTGTCT	539
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Qy	540	CCAGCTGTGCCACACTGGCTTCTCCCAACCGCACTACATCAATGGCCAGATGATCTG	599
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Qy	600	GTATGATATACAGCAAGCAAGAAATTTTGTGCGCTTTTGGCTACGGCATAGTCTGTAC	659
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Qy	660	ATTGCTGGCTTCT--TTCCCTCCTTGGTCAATTTTGGTGTGCTAATCACTGATGGTCA	717
Db	1004	TGTCATGGCTTCTGCTGCGCTTGTGCGCTTGTGCGCTGCTGCTGCTGCTGCTGCTG	1063
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Db	1064	CCGCTTGGCCGAGGATGGCCGAGAGCCTGTGGCCGAGCGCGGTGGCAAGGC	1123
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Db	1124	GGCCGCGATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1183
Qy	838	CAGTGTCTCTTCTACCTACCATCTGCTTCTGCTTCTGAGACTGGCCAGCTCTGTAT	897
Db	1184	CACCAAGACAGCTTACCTGGCAGTGGCTGAGCGCGGCTGCCCTGCACTGTATTGGA	1243
Qy	898	GGCAGCCAGTGTGGCTTACAGATATGAGGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGT	957
Db	1244	GGCCTTTCAGCGGCTTACAAAGCAAGCGGCGCTTGGCAGTGGCAACAGCGGTGTGGA	1303
Qy	958	CCCAGTCTGTACT	971
Db	1304	CCCCATCCTCTCT	1317

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Job time : 3909 secs

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